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4581	cg43993462	624	AGTCTCACTTCT TACCAAAAAA A[gap]A[CAATGA ACTGGATTTCAGC CCACTCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
4582	cg43928058	463	CCCACTGTGTGG CCCAGCTCTGG GG[G/gap]CCCTG CCTTGCCCTGCC CCTCCCTG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76081 STANNOCALCIN-2 - HOMO SAPIENS (HUMAN), 302 aa.	1.7E-160	
4583	cg43920504	134	ATGTATAATAAG AAATTCACCCCTT CIA[G]GCTCTAT TCACTCTTTATC CTGAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4584	cg43920504	626	TGTTCAATTTGG TTTTTCCATTTTC IACICGCAGAAA GGCCCTTTGTTG GTCTC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4585	cg43920504	636	GGTTTTCCATTT TCACGCAGAAAG IGTJCCCTTTGTT GGTCTCTGGTGT CAGC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4586	cg43134484	1242	CGAAGTGGCTCT CAGGGGCCAGT GA[G/gap]GGCTG GGCCACACAGAG ATGCATGCG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa.	5.8E-160	
4587	cg43134484	1398	GGGAGGCTCTTC AGTGGGTAGCT AT[C]TTGTTTAC ATGCAGATTTT GTAAT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa.	5.8E-160	



4588	cg43929687	173	TTGTAAGGGG GTGGGCTGTTGC C[C/gap]TGGCAC GGCTGGATGAAC ACTTGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa.	8.5E-160	
4589	cg43933630	574	GGTGCGAACGG TTCCGGGGCCTCA GG[C/gap]ACAGT GTGGGGGCCGC CTGCCCTCCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC-A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4590	cg43933630	677	GGCGGACCCCA GGCCGGCCCCAA GCC[C/gap]GACG CCAGGCAGAAC CCTTTGGGCG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC-A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5

4591	cg43933630	707	CCAGGCAGAAC CCTTTGGGCGG GGC[C/gap]GTAT CTGGCCCTCCG GGGACGGCAG	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4592	cg43933630	716	ACCCTTTGGGCG GGGCCGTATCTG G[C/gap]CCTCCG GGGACGGCAGT GACGACAC	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4593	cg43987224	406	CAACCATTC AAG GGTCAGGGCTCT G[C/gap]CTTCCC ACCAAAGGAGG GCCCCGAAC	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20

4594	cg43987224	407	AACATTCAAGG GTCAGGGGCTCTG C[C/gap]TTCCCA CCAAAGGAGGG CCCGAACA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20
4595	cg43987224	665	CTACAAGGGCAG CACTCAGTCTGC A[G/gap]CCCACT TGGGCAGGACA AAGCCAAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20
4596	cg42718246	1431	GCTGCATGTTTT CAACTACAATAA G[T/C]GCACTGTA ATAAAAAGTTTT GTTTA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13287 HOU - HOMO SAPIENS (HUMAN), 307 aa.	1.1E-158	2
4597	cg42831359	175	AGTGGGTTTTGG AACGGGAGGCA GA[G/gap]CATCT GGGACAGACC CTCCTGGAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa.	2.9E-158	1
4598	cg42831359	333	CCTGCCTCCCTG TGGGGGTCAGTT A[T/C]ACCCATCA GTCCTGTGCAAA GGTCC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa.	2.9E-158	1
4599	cg43923892	2095	AAATTACTCCTA AAAAGTTAATA T[C/T]CTGTAAA AAGCAATGCTTT TCAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AA45558 CYCLIN ANIA-6A - RATTUS NORVEGICUS (RAT), 527 aa.	2.9E-158	3
4600	cg42910688	1140	TCACCCAGATGT CCCTTTGATGGC C[G/C]TTGTTGAA GGCCATTGGGA CCAATA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8

4601	cg42910688	1389	GTGTTTCTTCTATG TTTGATAGTAGI G/A/GAAGTAAAG CTTACAAAGAAT GCCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4602	cg42910688	1926	ATGTATAATCAG AAGTCTGAATTT TT/CJATAAAACA TATAGCATAAAA ACTTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4603	cg42910688	1949	TTTATAAACATA TAGCATAAAACI T/CJTCCAGTACT TTGGTTGACCCCT TGTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4604	cg43272443	1395	AAGCTTTTTTTTT TTTTTTTTTTTTT gap/GAGACGGAG TCTTGCTCTGTT GCCC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4605	cg43272443	1461	TGCAGTAGCACG ATCTCGGCTCAC TT/gap/GCACCC TCCGTCCTCTCAG GTTCAAG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4606	cg43272443	1478	GGCTCACTTGCA CCCTCCGCTCTCT C/A/G/GGTTCAA GCAATTCCTCTG CCTCAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)

4607	cg43272443	1622	GCTGGTCTTGAA TTCCTGACCTCA G/GTTGATCCAC CCACCTTGGCCT CCCAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4608	cg43921539	1602	CCTGCTCAAGCG GTCCGGGGAAT GG/GTJTITTTGT TTTTCCCTTCATTG TTGAG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4609	cg43921539	3347	TGTTCAAGCTTT TTAAAGTGCTGA GT/CJCTTACAAA CCCCTGAAGGAA GGTGA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4610	cg43921539	3476	CCCAATTTGGTA AAATAACGGATC TA/GJATTAGAAA CTGTTTTAAGGA GGGC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4611	cg43984495	796	TGTTTAACCTCAA TGTAATGTGTAG ATCTAATACTTT TAGTGGGGTACA AGT	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20774 OSTEOINDUCTIVE FACTOR PRECURSOR (OIF) (OSTEOGLYCIN) - Homo sapiens (Human), 298 aa.	4.2E-157	9
4612	cg43048935	315	TACAAAACATGT AGAAGATGCCCTC TT/CJGAGATGGC TTTAAATGCCCC AGTAT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa.	8.8E-157	3
4613	cg43048935	664	GCTCTCTTCCTC TCTCTGTGCTTC AT/CJTAGAGGTA TAAATACTGGTA CATTG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa.	8.8E-157	3

4614	cg43953563	400	GCAGACTTGTGC TGGTCAGTGAAC A/C/A/C/T/T/T/T/T T/T/T/T/C/A/C/C/A/G/T CTGT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4615	cg43953563	414	TCAGTGAACACC T/T/T/T/T/T/T/T/T/T gap/T/C/A/C/C/A/G/T TGTGACATGGTG AATTA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4616	cg43953563	414	TCAGTGAACACC T/T/T/T/T/T/T/T/T/T gap/T/C/A/C/C/A/G/T TGTGACATGGTG AATTA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4617	cg43953563	597	ACAGTGTGAAC CCATACCTGTCA T/G/C/G/G/C/A/T/A GGAATGCATATT GATAAG	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4618	cg43953563	75	CATGAAGCCACC CATACAATCACA A/T/A/T/T/TATCTA ACACATTTAATTT TGA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4619	cg43254730	1016	TGAGATGAGGA ATTTAGAAGAT A/T/A/JATGAAGGC CTAAAAGATCAC TATCT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22
4620	cg43254730	279	TGAGGTATGGG GGTCACTGAGGA GA[C/gap]CCCCA GAGTCACTGACC CCTCCCCG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22

4621	cg43254730	283	GTATGGGGGTCA CTGAGGAGACC CC[C/gap]AGAGT CACTGACCCCTC CCGCCACC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22
4622	cg43329580	241	CTTGTCCTCCAGC CTGTGGGCAGT GC[C/gap]ACACG GCAGGCTAGGG GAGGGGTGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08742 SQV-8-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 327 aa (fragment).	3.4E-156	11 (11q13)
4623	cg43130238	188	AAAATTACAAAC AGCACTGATATT C[A/G]GCCAGTAT ACAAGTCTGGTC ACAGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21222 UBIQUITIN SPECIFIC PROTEASE UBP43 - MUS MUSCULUS (MOUSE), 368 aa.	7.1E-155	
4624	cg43950590	885	TTCTGGAGGGTG GGGAGAAGTGG CT[A/C]AGTGTTA TAAGGTATACTG GACAAAC	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.9E-154	7
4625	cg43981925	2094	ACAAAGGAACCGC TCGCCGCCGCC GC[C/gap]TCCGG TCACTGGCACGG ACTTCTGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4626	cg43981925	710	CACACACACAGA ATTTAAAAA [A/gap]TCAAAGG CAATCATTCTAA ATGTAC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4627	cg43981925	710	ACACACACAGAA TTTAAAAA [gap/A]TCAAAGG CAATCATTCTAA ATGTAC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8

4628	cg43981925	737	CAAAGGCAATCA TTCTAAATGTACT [A/T]TGATAGCAT GTAAAGATGCA AGTA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4629	cg43934638	966	GAGAAAGGAGAA GCTTACAAAAA AA[Agap]AAATC CTCTCTATATTG CAGTGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4630	cg43934638	967	AGAAGGAGAAG CTTACAAAAA AA[Agap]AAATC CTCTCTATATTG CAGTGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4631	cg43934638	968	GAAGGAGAAGCT TACAAAAA A[Agap]AATCCT CTCTATATTG AGTGCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4632	cg43934638	970	GGAGAAGCTTAC AAAAA A[Agap]ATCCTCT CTATATTGCAGT GTCTCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4633	cg43934638	1122	GGCTGAGTTTGT ATTATTACTGATA [T/G]GAAGAATAG AGTACCAATGTC ATTA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4634	cg43934638	1222	TTCTCAGATTG TAATTCCTCTTT [gap/C]GGGAGCT GAGCTAGTGCTT TTAGGA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5



4635	cg43934638	957	G TAGAACTGAGA AGGAGAAGCTTA C[gap/A]AAAAAA AAAAAAATCCTC TTCTATA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4636	cg43934638	958	G TAGAACTGAGA AGGAGAAGCTTA C[A/gap]AAAAAA AAAAAAATCCTCT TCTATAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4637	cg44001553	996	C CCAAGACCTTT AGCCCCCAAAGA G[G/gap]CACGGC CTCACCCCAACT GCCTGAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4638	cg44001553	167	A CTCAGGCAGAC TCCAGGGAGGA GG[A/gap]GGGG GTTCCACGGCTG ACGCCCAGG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4639	cg44001553	264	G AGGCAGGGAC CCAGGCTCCCAT CC[G/A]AGGTGG CCCCTGTACCTG CCCTGCC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4640	cg43247677	2273	T GATCCAATAAA GTTGTAAACAG G[C/A]AAAAAAA AAAAAAACAAAA CAAGA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14617 DELTA-ADAPTIN - HOMO SAPIENS (HUMAN), 1153 aa.	1.7E-152	19
4641	cg43928724	1932	C CTGGGCCAGG GTCTGTGTGAAT GT[G/gap]GGCAC TGGCCAGGTTTC ATACCTTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60539 PUTATIVE TUMOR SUPPRESSOR PROTEIN - HOMO SAPIENS (HUMAN), 289 aa (fragment).	4.1E-152	3

4642	cg43951092	104	TTTTTTTTTTTT TTATCTCCACA[ T/ATGACATTTAT TAATAACATTTCT GG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.5E-152	14
4643	cg43951092	291	TCTTTAAACTAA ACTCCAAGCAGG [G/T]ATCAGATAC AAAACCCCAACTG CAGG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.5E-152	14
4644	cg43930854	210	GCTCTATCCACC CCTACAGCTTCC C[C/T]GGCCAAC CAGGTTCAAAGC CCATCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4645	cg43930854	325	CCACAGAGAGA GGATGGGAAACT AG[G/A]GTAGAA GCTACAAGGGCT AAGAACT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4646	cg43930854	52	TTTTTTTTTTTT TTTTTTTTTTTT[G /T]TCACTGCAAA TTGTTTATTAAA CA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4647	cg43930854	5410	AGAGGGTTGGAA TGAAAGACTCCGA A[G/gap]CCACCA GGATGGGAAACA TGAGGCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4648	cg43930854	5410	GAGGGTTGGAAT GAAGACTCCGAA G[gap/G]CCACCA GGATGGGAAACA TGAGGCT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12

4649	cg43988751	180	CGGCTCCAAGAA GGCCCCCAAGG GG[G/gap]ACTTA CCTTCAGGGGG CTGAGCCAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4650	cg43988751	180	GGCTCCAAGAA GGCCCCAAGGG GG[gap/G]ACTTA CCTTCAGGGGG CTGAGCCAA	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4651	cg43988751	221	GCTGAGCCAAG GGGAAAGGGG TGG[C/gap]CCCA GAACAGGGGAA GGGCGAGGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4652	cg43988751	230	AGGGGAAAGG GGTGCCCCCAG AAC/A/GGGGA AGGGCAGGCA TGGGGGGAA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4653	cg43988751	43	TTTTTTTTTTTT TTTTTTTTTTTT[G /T]TGAAAAACCA AACCTCAAAAAG CCA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4654	cg43988751	45	TTTTTTTTTTTT TTTTTTTTTTGT[ G/TA]AAAAACCA ACCTCAAAAAGC CACT	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	

4655	cg43135797	400	GGCATGGAGCG TGGCCACGAG GGC[ <i>gap</i> ]ACCT CCCCAGGAGCC CACAGCAGCC	C	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.6E-150	18
4656	cg43135797	44	TTTTTTTTTTTT TTTTTTTTTTG[C /gap]CCATTATTT TGATTTATTGCAT TCT	C	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.6E-150	18
4657	cg43258297	60	TTTTTTTTTTTT TTTTATGGGGC[ A/GCGGGGGT CTTATTCGTCA GATT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa.	3.8E-150	3
4658	cg43919239	1089	ATGCTTTCTGT CCCTGCAGGCG GA[ <i>gap</i> ]/CIGCTGA ACCTCCGTTGCT GCTGGGAG	<i>gap</i>	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4659	cg43919239	1167	CTCTCTAAGTAG GCAATAGATCCA G[G/gap]CCCCCTA GGCTGTCCCCAC AGCCTCT	G	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

4660	cg43919239	1167	TCTCTAAGTAGG CAATAGATCCAG G[ <i>gap</i> ]/G[CCCCCTA GGCTGTCCCCAC AGCCTCT	<i>gap</i>	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR, (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4661	cg43919239	1174	AGTAGGCAATAG ATCCAGGCCCT A[G/ <i>gap</i> ]/GCTGTC CCACAGCCTCT GTCTTCG	G <i>gap</i>	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR, (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4662	cg43919239	1175	GTAGGCAATAGA TCCAGGCCCTA G[G/ <i>gap</i> ]/CTGTCC CCACAGCCTCTG TCTTCGG	G	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR, (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4663	cg43943351	1714	GGGTGGGCGAG ATTCTGGACTGA GG[ <i>AT</i> ]/GGGCAG GGGAGGGAGAA AGGTGCTC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17
4664	cg43943351	1880	ACTGGGGCTGA GCCGGGCCCTC CAG[G/ <i>gap</i> ]/CTCA TGCCCGGCTGC AGGTGAACAT	G	<i>gap</i>				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17

4665	cg43946935	162	ACCGCAAGGTG TTTGGCGATCCG C[C/gap]GAGAAG TTGTTGGCCCCA GGAGCAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60671 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa.	1.8E-149	
4666	cg39524115	1245	TTCTCTGCCTC AGCCTCCCAAGT A/A/G]CTGGGATT ACAGGCACGTAC CACCA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4667	cg39524115	1385	CCCGCCTTGGC CTCCCAAGTGC TG[G/A]GATTACA GGCATGAGCCA CCACGCC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4668	cg39524115	1391	TTGGCCTCCCA AGTGCTGGGATT A/C/T]AGGCATGA GCCACACGCCT GGCCT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4669	cg43930377	718	CAATGTTGTTTAT ATAAGTATACCA[ C/gap]ATTATAAG TCTACTGGAGAT CCAAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
4670	cg43917492	1706	CGCCCAAGTGAC TTGCTGAATACC A/T/C]CACAAAAT CTGAACCCAAAG ATGAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4671	cg43917492	2086	ACTTTCATACTG GTTATTTTTTTTT T/gap]TAATTCTG TCAGTGAGCAGC ATTTC	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4

4672	cg43917492	2087	CTTTCATACTGG TTATTTTTTTTTT T/gapJAATTCTGT CAGTGAGCAGCA TTTC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4673	cg43917492	2087	TTTCATACTGGT TATTTTTTTTTT gap/TJAATTCTGT CAGTGAGCAGCA TTTC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4674	cg43917492	3146	CGAAGCACCGTT GCTCGGAGCAG CC[C]gapGGCGG GGAGCAGGAGC TCAGGGACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4675	cg43917036	1328	AGCATCCCAGAG AAGCTCTGTCTG C[G/A]CTGCAAA GCCATGGCTGCA GACATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa.	1.3E-148	8
4676	cg43041577	2015	TGAAACCAGAAT CTTTTTTTTTTT gap/TJAATCTGTA AATAGGTGTACT TTTT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.7E-148	10
4677	cg43943919	68	GAGTCAGAACAT TAGACTTATAGT G[G/A]AGGAGCA GAACGAACCCT GGCCTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa.	2.7E-148	X
4678	cg44921374	1526	GAAAAATTCTCT CTCAAAACAAAA C[A]gapJAAAAAA ACCTACACACAA CTGAGTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148 (12q23)	12

4679	cg44921374	1652	ACAAATGTA GTTCTTTTGT [A/gap]AAAAAGG GGTAGGATTAG GTTCA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4680	cg44921374	1662	TAGTTCTTTTG TTAAAAAGGGG [G/gap]TAGGATT AGGTTTCATATA TTAAAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4681	cg44921374	2203	TGCATTTTCAGC AATATTATCGCC A[C/gap]AGACTC TGATTGCTCAGT CCACACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4682	cg44921374	400	AGTTCAACTGTT CTCAATCTATGC TTA/gap]AAAAAAA AAAAATGACAAA TAATAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)



4683	cg44921374	412	CTCAATCTATGC TAAAAA A[A]gapJTGACAA ATAATAAATTCTA CATTTC	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4684	cg44921374	412	TCAATCTATGCT AAAAA A[gap]AJTGACAA ATAATAAATTCTA CATTTC	gap	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4685	cg44921374	539	AGCTGTAACCTCA GTGTGGTTTTC A[G]AJCTGCCTAC GTTAGTACCAGG TATTTC	G	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4686	cg44921374	583	GGTATTCATATA AACTCTGTAGAG G[C]TCATTACAA TTTCGTAAATTCT GTAA	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)

4687	cg44921374	786	AATCAACTACTG ATCATAACAGCC C[A/C]ATTAAAA CTCAAAACACTT ATATT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4688	cg44921374	855	ATCCAGCAATGC CAATATAGGTAA TTT[C]TGATAGCC CCTATTGCAAA GTGAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4689	cg43927534	317	TGATGTGTCAIT CTCCCCAGCAG GG[G/gap]AGGG GGTGAATGGCT TGGTTGTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9E-148	1
4690	cg43965796	131	CAAAAATTCACA GCGCCTGTGAG GA[G/gap]CCCTT GGCTGGAACTG GTGACACCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4691	cg43965796	383	AGCACCTCTCCC AGCTCCAGCCCCA TTC/TGGCTGGA GAGGAAAAGGG CAGAAAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4692	cg43965796	462	CACACCTACTAC ACAGATGATAAA A[A/gap]TCCCAC AATCGTATCTGT TCATGTT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1

4693	cg43965796	902	TGCTGTAGGCCT CCTCGAACATGG C[C/gap]TTGCAG GGGAAGCGGGC CTTCAGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4694	cg43942977	1171	TTCTCTCCAGC AGCCTGGGGG CA[G/gap]GGCAG AGCCTCCAGTCG GACCCCTT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.6E-148	
4695	cg43942977	1173	CTCTCCAGCAG CCTGGGGGCA GG[G/gap]CAGAG CCTCCAGTCGGA CCCCCTCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.6E-148	
4696	cg43261322	1073	ATGTCACATTTT TGATTCTAGCTA C/TCTGTATTAT TCACCTAGCTTG TCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa.	5E-147	12
4697	cg43261322	2207	CCAGAAAACCCAC CAATCGGCTTTC A/T/ATTTGCATT TTGTAGTTTATG TGAA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa.	5E-147	12
4698	cg43985545	134	AGAGCAGAAAG GGACACCTCCAT AG/ATGTGTCTA TGGACCCCATTTT TGCTTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA08666) - Homo sapiens (Human), 274 aa.	6.3E-147	6
4699	cg43985545	292	CATCAGCCTATC AGGAAATCTGAG G/GA/GAGGCAG ACAACCCAGAAGG AGAGTT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA08666) - Homo sapiens (Human), 274 aa.	6.3E-147	6

4700	cg43985545	313	GAGGGGAGGCA GACAACACAGAAG GA[G]A[AGTTGCT TCCTCTCTCACC AGGAAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA0666) - Homo sapiens (Human), 274 aa.	6.3E-147	6
4701	cg42718779	1443	GGGCTGAGAAT GAACCTGACTAG AG[C]G[TTCTGGA GATACCCAGAGG TCCCCC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O75712 GAP JUNCTION BETA-3 PROTEIN (CONNEXIN 31) (CX31) - Homo sapiens (Human), 270 aa.	1.4E-146	1
4702	cg43937734	1520	GGTTCCTGCGCT CCTTCTGGTGCT C[C]gap]TACTCC AAGTCTATTTCAT TTTTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4703	cg43937734	2139	TCCTAGTATTTT CTTACCTGAAG[ G/T]AGGGCCATT TATTTTAAATTC ACT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4704	cg43937734	561	CTCGCTGACCTA ATAAGGCCATGC A[gap/A]GTGTGC GGGGGAGCTAC ATAAAGC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4705	cg42924529	168	AGTCTGGGACTC CTGGCCCTCCAG G[C]gap]CCCTCC TCTCCAGAGAC CCTGATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa.	3.1E-145	

4706	cg42924529	186	CTCCAGGCCCT C CCTCTCCAGAG A[C]G[C]CTGATG CAGCTTGTGGC TGGACC	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa.	3.1E-145	
4707	cg43961927	165	TTATTTTAACCCA C GGCCAGGGAG G[C]gap]GAAGCT TCAATCCTGCTG CTTGGTT	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
4708	cg43961927	165	TATTTTAACCCA GGCCAGGGAG GC[gap/C]GAAGC TTCATCCTGCT GCTTGGTT	C gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
4709	cg43985220	2180	TAATTAACCTTCAT C TGCCGCTGGATT [C/A]TGTTCAGCC TTTAAAAATATTT CTT	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8

4710	cg43985220	2369	GTGTTGTAAAT TAAAAATGCTTC TGAATAAGTTT TCAAGGTAGGGA GTGAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4711	cg43985220	2420	TTTATTATTGTGT ATATCTAATATA[ T/gap]TAAGTATG TGTGATACTAAG GTTTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4712	cg43985220	2421	TTTATTATTGTGT TATCTAATATAT[ T/gap]AAGTATGT GTGATACTAAGG TTTGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4713	cg43269627	319	TTTGATAATAAGA CAACCTTGTGAT[ A/GTCTATTCAA GAAAAGCCAGAG CCCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15404 RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) - Homo sapiens (Human), 277 aa.	1.1E-144	10
4714	cg43256169	289	CTGGGTGCCGC ACAGTCTGCTCC CT[G/C]GGGACA GAAACCCACAGG GTCGAGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	

4715	cg43256169	401	GGGAGGGCACA CAGGCTGGGTG GCA[C]gap]CCAG TGGCCAGGCC CTTAGCTGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4716	cg43256169	414	GGCTGGGTGGC ACCCAGTGGCCA GG[C]gap]CCCTT AGCTGGGCCGC AGGCAGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4717	cg43256169	428	CAGTGGCCAGG CCCCTTAGCTGG GC[C]gap]GCAGG CAGCACTGAGCC GCCTGGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4718	cg43983449	945	CCCTGAAAAGAA ATACACAGCCTA GT[G]CATAGTAT ATCATATAAAGG TTATT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4719	cg43983449	952	AAGAAATACACA GCCTAGTCATAG T[A]G]TATCATAT AAAGGTATTTT CTTAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4720	cg43983449	1041	TCCATAGTCCC TTACTAGGCAGT G[C]gap]CACATA AAGTATTTAGTT AACATT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4721	cg43983449	343	CATAAGACAATG GAGCTTTAAAA A[gap]A]GGTTAG GTTTACATCTTT AAAACT	gap A	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	

4722	cg43983449	650	GTCAGCAAAATG CCTTTGACTGAC G[C/gap]CCTGGA TTATTTTACCACT TAACCT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4723	cg43983449	899	ATGGTAATAGTA ACTAAACTACAT C[C/T]AACCCCTGA AGGTAGAAAAAT CCCTG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4724	cg43983449	931	GAAGGTAGAAAA ATCCCTGAAAAG AATATACACAG CCTAGTCATAGT ATATC	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4725	cg43925411	61	AAACAAAGGTAC CAGTCGCCGCC GC[G/gap]GGAGG AGGAGGAGCCG GAGCCTCTG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	9.5E-144	10
4726	cg43971525	103	ACCTCTGAAGTA AGGCACAAACACA AT/CJTCCATTGT CACTGTGGCAGA AGTCC	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
4727	cg43971525	181	AAGACTGTGGTC CACGGGCCCTAA GG[C/gap]JACTTG AGCTTTTCCCTC AACTGAAG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
4728	cg43971525	322	ATGAACATCAAG AATTACTAGACA T[G/T]TAAAAGTG TCITTAAGTGTC TTTCC	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11



4729	cg44027658	1145	TGAGAGAAATT GAGATGTGTA A[A/gap]TCTAGTT ACTGCCTGTAAA TGGTGT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4730	cg44027658	191	GGCCTCGGCA CCGCGTCCTGTG GG[G/gap]CGGCC GCCTGCCTGCC CGCCCGCCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4731	cg44027658	227	CCTGCCCGCCC GCCCCGAGCCC CTT[G/C]GCTGC CGCCCCCTGGG CGGCCGCTG	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4732	cg44027658	228	CTGCCCGCCCC CCCGCAGCCCC TTG[G/C]CTGCC GGCCCCCTGGC GGCCGCTGC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)

4733	cg44027658	249	CTTGGCTGCCG GCCCCTGGCG GCC[G]CTGCC ATGGGCACCGA CAGCCGCGC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4734	cg44027658	250	TTGGCTGCCG CCCCTGGCGG CCG[C]GTGCCA TGGCACCGAC AGCCGCGCG	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4735	cg43999829	1084	GAAGCAGGGCC CTGACTGCCCCC CC[C]gap GGCCC CCCTCTCGGGCT CTCTCACC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)
4736	cg43999829	1198	TAAATGCAAAGC ACACCTCGGCC GA[G]gap GCCTG CGCCCTGACATG CTAACCTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)

4737	cg4399829	1199	AAATGCAAGCA CACCTCGCCG AG[G/gap]CCTGC GCCCTGACATGC TAACCTCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2 )
4738	cg43917524	372	CTTCCCAGTCTT TTTTTTTTTTTTT T[gap]GAGACAG GGTCTAGCTGTC ACCCAG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43025 PTD017 - HOMO SAPIENS (HUMAN), 258 aa.	3.2E-143	
4739	cg44000122	153	CAAAAGGTGGCAA ACATATTTATTGC [C/A]TCACTGTAA ATAGAGAAAATC TTGT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4740	cg44000122	389	GCAGCTGTGCTG TGATTATGAGAC A[G/A]ATACAAATG ATTCACTACCTGGC TGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4741	cg44000122	968	AGACGGTGAAG GATTCCACAGCC AG[G/C]GCTGTAT TAGCAGCTAGAG CGATGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4742	cg44020482	132	GGCAGGGCGGAC CCAGCCCCCGG GGG[G/gap]ACAT GAGGGCCAGGG GAGGGCAGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92561 HYPOTHETICAL PROTEIN KIAA0273 - Homo sapiens (Human), 330 aa.	2.9E-142	8

4743	cg43334997	1155	CTGCGCTCTGAG ATGAGCTGCCCT C[G/C]GCTCCCT CCGGGTGGCG CGCCCGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75973 C1Q- RELATED FACTOR - HOMO SAPIENS (HUMAN), 258 aa.	2.9E-142	
4744	cg43958563	172	ATGACTGTATTT ATTTGTACAAAA [T/C]GCAGTAACA CTTCTCTTTTCC TCT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4745	cg43958563	341	AGTGGGAATGA AAACAGGCAGAG G[C/gap]CAGCAG GTTCTCGGCTA GGGCTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4746	cg43958563	354	AACAGGCAGAG GCCAGCAGGTTT CT[C/gap]GGCTA GGGCTCTGCCTA TAACGCCCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4747	cg43958563	368	AGCAGGTTTCTC GGCTAGGGCTCT G[C/gap]CTATAA CGCCCTGGTCCT GCTCATC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4748	cg43958563	369	GCAGGTTTCTCG GCTAGGGCTCTG C[C/gap]TATAAC GCCCTGGTCCTG CTCATCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)

4749	cg44964063	1636	AAATACAGTTAA ATGTGTTATTTG C[T/gap]TTTTAAAA TTATAAAAAGCA AAGAGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa.	6E-142	10
4750	cg44964063	1639	TACAGTTAAATG TGTTATTTGCTTT [T/gap]AAAAATTAT AAAAAGCAAGA GAAGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa.	6E-142	10
4751	cg43951474	1863	ATGGCTCTGCT GTCCTTCCCCAG T[C/gap]CACCAG GGTGGGGGGA CAGGGGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4752	cg43951474	1864	TGGCTCTGCTG TCCCTCCCCAGT C[C/gap]ACCAGG GTGGGGGGGAC AGGGGCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4753	cg43951474	1918	AGTGCATTCATT TTGTGCTTTTCTT [G/A]TGGGCTTTC TGCTTAGTCTGA AAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4754	cg43973724	2810	GCTTTATTCAA CTAAGGTACTTA C[C/T]AAAACCTT AGTTTTATACA GGTGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.3E-141	1
4755	cg43119818	1895	AGCCCTGCTTCT GACATAATCCAG T[gap/T]AAAAATAA TAATTTTAAAGAA ATAAA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.9E-141	8 (8q22)

4756	cg43119818	2057	TAGTAATCTGTA AGCATAAGCTTA T[G/gap]CTTAAAT TCAAAGTTTAGTTT GAGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.9E-141	8 (8q22)
4757	cg43919223	206	ATCTTTTCTTAC AGGATTCTTACC[ G/T]CAGGAATAG ATGGACATGGCC TGCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa.	1.4E-140	11
4758	cg43328633	3746	CCTCAAAGCCAG GTGCTGGCCAAA T[A/G]CCTTGATC ACAGCCTCCATG GCCAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15049 HYPOTHETICAL PROTEIN KIAA0341 - Homo sapiens (Human), 546 aa (fragment).	1.5E-140	
4759	cg43922710	125	CTCTACCCAGCT AAATACACATTAT [G/gap]GCATTTA GCAAACTAACTT ACAAGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment).	4.9E-140	
4760	cg43935709	449	ACAACAACATA TTTTGGACAAAA C[A/C]ATTTTTTT TAATCTGCTTG TAAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4761	cg43935709	505	TACTTCCTTTTGA GTCTCTGATGGC [C/T]ACAACATTT CAITTGAGATGT TTGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4762	cg43935709	695	TGCCCATGGTGG AAATGCTGGA A[A/T]TTAAAGGT AAGAAATAAAC ATAGC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20

4763	cg43935709	92	GATGGATAGATT TTTTTTTTTTAA[ A/G]GAAATTAGC CTCCCTGGGTAC TTAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4764	cg43935709	941	TCCTGCTTGGCT TTCATTTACAG G[G/gap]CCTGCA GCCTTGTCCTG GAAGGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4765	cg43950100	927	AGGATGGAAG GTGGAAGGGTAA AT[G/A]GCACAG GGAGAAAAACAA AGTGTTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.7E-139	11
4766	cg44030891	368	CCCCAGCCCTG GCTGCCCTCTGC GG[C/T]CCCCAC CCAGCCCTGC CCCTAGGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99750 MYOGENIC REPRESSOR I-MF - HOMO SAPIENS (HUMAN), 246 aa.	2.1E-139	6
4767	cg43936172	355	ACCTCATGTCTC TGGGCCGGGAA GC[C/gap]ACGAT CCCTCATCCATC AGGCCTGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60429 F17127_1 - HOMO SAPIENS (HUMAN), 528 aa.	2.7E-139	19
4768	cg43917807	1667	ACTCCTTTAGGC ATGCAGGTAAC G[gap/C]CCCCCA CGCCCCCCCCGC CACCTCCC	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4769	cg43917807	466	GAGAAGATTAAAC AAAGTCCCTTCT T[C/T]CAATATCA GGATAGTCATGA GTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17

4770	cg43917807	467	AGAAGATTAACA AAGTCCCTTCTT C/C/TAAATATCAG GATAGTCATGAG TTGCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4771	cg43917807	564	GAACATATGAGAT TCCTGCTCCCTC C/G/gap/GGGGAG CCAAGGAGCTTG CAACTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4772	cg43917807	723	AGAGAAATGGACA GTGTGATCCTTG T/T/C/JTGTGCTAG CCATTGGGTGAT GCACC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4773	cg43285114	427	GCGGGCACCCCC GTGGGGTCTTTG GC/G/AJGCTCAC AGGACAATGGCA GTGGAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD23440 LR8 - HOMO SAPIENS (HUMAN), 270 aa.	1.9E-138	7
4774	cg43303845	271	TGGTGTAGCCCC CTGGCCGCCCGA AG/G/gap/JAGGAG CCGGACACTTGT CTCCCGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O83263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.9E-138	
4775	cg43992302	1911	CATTCTCTCATTG TTTCATGTTTGA C/C/TJTAAAGGT GAAAAAAGAAAA TGGCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa.	4.5E-137	4
4776	cg43992302	2082	TTTGCATAAATC ATAAATGTATGT C/C/TJCTCTGTA ATTGTTTTAATGT GTGC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa.	4.5E-137	4



4777	cg43935076	229	CCAACCCCAAAG CATTTTGGGTT C[A]G]GCCAAGC CAGACAAGGGA CCCACAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4778	cg43935076	409	AAGTGAAAGTT TGGGTGGCGTG GG[C]gap]CTCAT GCCACACTGATT GGTCAGTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4779	cg43935076	410	AGTGAAAGTTT GGGTGGCGTGG GC[C]gap]TTCATG CCACACTGATTG GTCAGTAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4780	cg43935076	443	ACACTGATTGTT CAGTAGACAGG GG[C]gap]CACAT GCCAAACACCAC AGGCATC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4781	cg43935076	450	TTGGTCAGTAGA CAGGGGGCACA TG[C]gap]CAAAAC ACCACAGGGCAT CAGATGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4782	cg43935076	451	TGGTCAGTAGAC AGGGGGCACAT GC[C]gap]AAACA CCACAGGGGCATC AGATGCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4783	cg43935076	629	ACACTGTTTAA GCAGTAIGTTTA A[T]C]TGGATGAT TTCCACAACACTA TCCAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1

4784	cg43935076	643	AGTATGTTTAATT GGATGATTTCCAA C/TJAAACTATCC ACGAAGTTTCTA ACCA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4785	cg43952219	675	CAGTGGTTAGTA TTTTTTTTTTTT T/gap]CCTTTTTT TAAAGCATAAGC AATAG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
4786	cg43922796	692	CAGGGCACCCAG ACAGCAGCGGC CCCTT/CJTTCCTCA GGAGGTACAGG AGACAGGA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q00004 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) - Canis familiaris (Dog), 622 aa.	3.2E-136	1 (1q42)
4787	cg43947491	537	AACTTTAATTGA ATGAGAAATACA T/CJCTGTCAAAG ACCTGGGCAGTA CACT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P30040 ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28) - Homo sapiens (Human), 261 aa.	1.8E-135	12
4788	cg43994220	136	TGCCCTTTGAAGT CAGTCTGGGTT T/C/gap]CCCCAGC TCTGGCTGACCA TTTTGTT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
4789	cg43994220	186	TCCCTGAGTGTC TGAGTCCCCGG CA[G/gap]GCGGC CTTCACTCAGGG TCAGCGGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
4790	cg43994220	187	CCCTGAGTGTC GAGTCCCCGGC AG[G/gap]CGGCC TTCACCTCAGGGT CAGCGGGC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19

4791	cg43948495	1584	CGCGGAGCGTG CGGTCTGGACCA CQ[C/gap]AAGGG AAAACCCCTCAT TTTAGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4792	cg43948495	1623	TCATTTTAGCAC AGCGGCCTGG GC[T/A]GCGTCC AAGCTCTCGTAC TGAATAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4793	cg43948495	1649	GCGTCCAAAGCTC TCGTACTGAATA T[A/G]GGCAAAG CTATCTCCTTTG ACGTGA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4794	cg43948495	1707	TCCGAATGCTCC CAAAGCGGTCAA A[C/T]TCTCGGGC CAGAGCCGCCA GTGACG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4795	cg43948495	1708	CCGAATGCTCCC AAAGCGGTCAA C[T/C]CTCGGGC CAGAGCCGCCA GTGACGT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4796	cg43948495	2526	GAGGCTGATCTC GCCGAAGCGCTT G[gap/G]AACTGG TGGAAGAGCCG GTCCTCGA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4797	cg43948495	2567	CGGTCCTCGAG GTGCTCGGCGG GCA[G/T]CGCGA GGGCCAAGGCG CCGGGGGACG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3

4798	cg43948495	2573	TCGAGGTGCTCGG GCGGGCAGCGC GA[G/C]GGCCAA GGCGCCGGGA CGCGAATC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4799	cg43948495	2579	TGCTCGGCGGG CAGCGCAGGG CCA[A/C]GGCGC CGGGGACGCGA ATCACGCG	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4800	cg43948495	28	TTTTTTCAGGT TAAAAATCCATC C/gap]TCTGTCAA AGGTTTACTGA CAACT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4801	cg43948495	31	TTTCAGGTTAA AAATCCATCCTC T[gap/C]GTCAA GGTTTACTGAC AACTTTC	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4802	cg43948495	409	CTAGCTTGCCCA ATGTCCCTTAGTG CT[A]GACTGGA GGTACTGCTGG GAAAAGT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4803	cg43948495	463	GGGTGGGAAGG CGTAGAGCATGC CT[gap/T]GTGCC GTCTCTGCCCTT GGACCCCC	gap	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4804	cg43948495	510	CCCCCACTGG CAAGCTGATCAC CC[C/gap]TCCGG CCTGCTTCTGTT TCAAGTAG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3

4805	cg43916993	1938	ATCCGCTTGATT CCACTTGGTTTT GTTAAAGTTTT CCAAATCTTTGG AGAGT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4806	cg43916993	833	CCCACAAAGGG GGACGATCACG GCC[C/gap]AGCA AAAGCGATGCTG AGAGGGGAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4807	cg43916993	855	GCCCAGCAAAAG CGATGCTGAGAG G[G/A]GAAACAG TCCAGAGTCCAA CAGCAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4808	cg43916993	945	TATGTATAGGG CCGGGGGCTTC TG[C/gap]CCAGG GCTCCCTGGAC CAGGACGC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4809	cg43916993	947	TGTATAGGGGCC GGGGGCTTCTG CC[C/gap]AGGGC TCCCCTGGACCA GGACGCCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4810	cg34758981	1158	TTTTTATTAATAC AAGTCACITTTT A/C/AAAAATTTG GATTTTTTATAT ATA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48307 TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR (TFPI-2) (PLACENTAL PROTEIN 5) (PP5) - Homo sapiens (Human), 235 aa.	1.6E-132	7
4811	cg42910848	281	GACAGGTGTGG GAGGTAGCTCGA AA[C/T]ATACAGA GTGTTCCGAACA CTAGAG	C	T				SILENT- NONCODING 886	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.1E-132	

4812	cg42910848	295	GTAGCTCGAAAC ATACAGAGTGTT C[G/A]CAACACTA GAGACGTCCTCT GGCTG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.1E-132	
4813	cg43317146	162	CAGCTTTGCTGA AACTGTACTTTG G[G/A]CTCCAGA CTTCACTGTCCT TAGGCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4814	cg43317146	81	AGATTCATTTTCT TGAGTGGCACTG [C/gap]CATGCTC ATTCAGTGAAAA CTTGTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4815	cg43317146	82	GATTCATTTTCTT GAGTGGCACTG C[C/gap]ATGCTC ATTCAGTGAAAA CTTGTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4816	cg43957878	85	TCCACTACAAA AATACAGAGGAG A[T/C]AGGGTGTT TCCTGTATCCGC CTCAT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99753 CISPLATIN RESISTANCE ASSOCIATED BETA PROTEIN - HOMO SAPIENS (HUMAN), 252 aa.	7.1E-132	1
4817	cg43087636	1059	TTAAAATTATTTC TAGGAAAGTCAAA T/A/AAATATAATA AAGGGTTGAGCC CTC	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa.	1.5E-131 (14q22.1 )	14
4818	cg43087636	1145	AAGTGAACGTGCT AATAGTGTAAAGT A[C/T]GTGCACAA AACCAGTCCAG ATAAC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa.	1.5E-131 (14q22.1 )	14

4819	cg43087636	1314	TTTCTTCCTCCA ATAAAAAGTGGTG T[A/G]GTGCCGA AAGTGCTAAAT ATTAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa.	1.5E-131	14 (14q22.1 )
4820	cg43918679	1275	TGCCTGTCTACA CCAGTCCTGTCC C[C/gap]AGGACT CCCTTCTGTGG TCTGGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
4821	cg43931621	1023	GCATTAGAATGC TGGATGAGACTT A[A/gap]AAGCTT CAGTTCACTGTA AAACTA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4822	cg43931621	1025	ATTAGAATGCTG GATGAGACTTAA A[A/gap]GCTTCA GTTCACTGTAA AACTAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4823	cg43931621	760	AACCGTGTCTAT AATTTTTTAAAG [G/A]AAAAAACCT GCTTTCCAAAC TTAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4824	cg42859936	185	TACTTGGAAATAC ATGCCATTATCT C[T/C]GCATTTTA CAATAAGAAAT CATCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99644 DELTA SARCOGLYCAN - HOMO SAPIENS (HUMAN), 256 aa.	8.1E-131	5 (5q33)
4825	cg42382358	1842	CTCCCCACCCAC CACCCTCCCG CG[G/gap]CAAGC CAGCCCGTGCA CGGAAGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa.	5.7E-130	4 (4pter)

4826	cg43946922	1714	GGTCCGAGGAC AGAAAGCGCCG GTG[G/gap]CGGG ACGCAGGGGAG GCAGGGTGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4827	cg43946922	735	AGAGATTACAA CAATTTAAAGA C[A/gap]AAAAAA AAAAATGGTCCTA TTATGTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4828	cg43946922	745	AACAATTTTAA GACAAAAA A[A/gap]TGGTCC TATTATGTGGTC CCAACAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4829	cg43928955	225	GGCGAAGAGCT GGGTCCTGCAG CTC[C/T]GGTGG GAGCCTCCTCAG TTCTTTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4830	cg43928955	254	GGGAGCCTCCT CAGTTCTTTTCG GAT[C/G]GCACTCC ACCCCCGCGAAT CCGGTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4831	cg43928955	315	TGCGGAGAGCG GGCTTAGTGCC TC[G/C]CCGGCT TCGTGGCCTCCC AGGCTTC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4832	cg43928955	337	CTCGCCGGCTTC GTGGCCCTCCCA GG[C/T]TCGCTC TGACCCCTGTCTG GGCTGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	



4833	cg43928955	364	TCGCTCTGACCC TGCTGGGCTGG AT/CJGGAGGCC GGACCGCCCTTC CTGGCG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4834	cg43928955	460	AGGATAGACGG GCGGGTGACCC GTG/A/GJCCCG TACCCACGAGTT TGGGTCC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4835	cg43928955	486	CCCCGTACCCAC GAGTTGGGTCC C/T/CJTGAGGCAT CTCTCCAGGCCT CTGCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4836	cg43928955	667	TTGAGAACCCCTC TCGAGGAGTCTG G/C/GJCTCATGA GGATGCCAGAAC AAATGG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4837	cg43950545	203	ATCCCCACAAC AGATAGAATGAA TT/CJTTTTTAGG AGCAAATGACAT GCITT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	3.5E-129	13
4838	cg44938448	103	AAGAATCATAGA CAGCTACTACCA C/G/AJGCTGCTTC GTTTGACAAA ATAAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4839	cg44938448	963	CATGTAAAAAGC TGCTTGTTGGC C/C/TJGTTATCC CACTGACCCGTC TGAGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1

4840	cg44938448	1149	CCATGGTAATTT TTCACAAATTAAA [A/G]ACACATTTT GGGTTGTGCAAC AGTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4841	cg44938448	129	GCTGCTTCGTTT GGACAAAATAAA C[C/G]AGGAGGC ATCCACGGGATT AGTTAC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4842	cg44938448	1264	TTTTCTTTTAA CCTTTTATGCC[ T/A]TTCAGTAGG GGAAGTTTCCTT GAAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4843	cg44938448	1311	GAAAGTTAGAGA GCTGCAAAATCTC TT/gap/AAGTATC AATGTAAGAAG CAGATG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4844	cg44938448	1321	GAGCTGCAATC TCTTAAGTATCA A[T/C]GTAAAGAA GCAGATGACCCA ATTGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4845	cg44938448	1332	CTCTAAGTATC AATGTAAAGAAG C[A/C]GATGACC CAATTCGGAAGG TGGTTC	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4846	cg44938448	166	ACGGGATTAGTT ACACGGTATCAA CTT/CJTACCACCA CAGCAGAATCAA CAGTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1

4847	cg44938448	6409	CGCGGCTGCCC GTTGGTTCCGCC CG[A/G]GCCGTT CTACTCCAGGCA GACGGGA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4848	cg44938448	6463	GAAACACGGCG CCTCAGCGTCCC CT[G/C]CCCCGTT GGTCTGCTCGG GCCCTT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4849	cg43972431	1024	GAAAAGTTTAA CACTGGAGAATT C[G/A]CTATGGTG AGCCTAAGCAAT ATATA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa.	7.1E-129	2
4850	cg43931286	1069	GGATGTAGTTCC TTTGTAAGGGTG G[G/gap]CAGGCC TCGTAAGAAAGA TGTAGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa.	1.4E-128	17
4851	cg43298916	116	GCTATGGCATCT TTAATTATAAAAA [gap/A]TAAGCAA ATAAATAACTT GCATCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4852	cg43298916	193	TTTATATGCACAT GGAGCTTAAAAA gap/A]TGTAATTT AACAAATAATAAT GACA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4853	cg43298916	2603	GTGGTCTCAGG GGAGCAGGGGA AAA[gap/G]ACAT GGCAGAGGAAG TTGGTAAAG	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8

4854	cg43298916	425	ACGAAGCTTTGG AAGTTTAAGGG G[ <i>gap</i> ]/G[ <i>gap</i> ]AATTGG AGGGAGTAGGG TGGGGAA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4855	cg44128041	940	ATATATTATGG CCGGGCAGGGT GT[G[ <i>gap</i> ]/GGGCC ATGCCTCCTCAG GAGCCGAA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4856	cg44128041	943	TATTATGGCCG GGCAGGGTGTG GG[G[ <i>gap</i> ]/CCATG CCTCCTCAGGAG CCGAAGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4857	cg44128041	1082	TGCAGGACCTCG TGCCACCCCGA GG[G[ <i>gap</i> ]/CTGAG CCTGGTCCCACG AGGGTGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4858	cg44128041	1115	TGGTCCCACGAG GGTGCCCGTGT CC[C[ <i>gap</i> ]/TGACA GGGCCAGTGCA GTTTGGTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4859	cg44128041	1153	TGCAGTTTGGTG TGTCCTCCGCCT TT[A]CCAGGAGA AGAACCTGAAGA ACTAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	

4860	cg42891437	989	GGGACAGGGC CTGGAGTCAGAG CTGTGGGGC GTGAGGGCGA AAGGGGAC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127	7 (7q21)
4861	cg42891437	991	GGACAGGGCCT GGAGTCAGAGCT GGGTGGGCGT GAGGGGCGAAA GGGGACAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127	7 (7q21)
4862	cg43995142	110	GTTTCTCATTTTG TTAAGCTGCAA[ G/gap]CAAGTTTC TTTCACAATTACA CTTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa.	8E-127	
4863	cg43949897	913	GGAGCCACCAA GCACTTTGAGC TG[G/gap]CCTCG CCCCTAGGAG GAGAGGGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa.	1.8E-126	19
4864	cg42549778	1633	TGTGTGTGTGCA CTGCTGTGTGTG T[gap/G]TGCACG CACAGGAAGCCT TTCCACA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa.	3.7E-126	
4865	cg44002192	1646	GGACTACATCTC CCAGCCCTTCAC G[C/T]GTTAAATA TGAGTGGTTTTA AAAGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16
4866	cg44002192	2337	AAGACCTTCAGT GTAGATCCAGAT G[G/C]CCCAACCT GTCCTTGTTAAG TTACTT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16

4867	cg44002192	2876	ACTGGTCATCTC CTGAGGACCTGT A/C/A/TAGACCT GTGGACTGTTCC GCACG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16
4868	cg43949061	863	GCCCGGGAGTG TTCCGAACGGAG CTG/C/GCTCCG CCACGCCCACTG CTAGCCC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
4869	cg43307940	36	TTTTTTTGATTTT TTTTTTTTTTT[G /TGTAGCATAGT GAGTGGAGTTTA TTT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4870	cg43307940	37	TTTTTTTGATTTT TTTTTTTTTTT[G G/T/TAGCATAGT GAGTGGAGTTTA TTTT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4871	cg43307940	46	TTTTTTTTTTTTT TTGGTAGCATAG[ T/A/GAGTGGAGT TTATTTTATAAT TTG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4872	cg43307940	887	TGTCAGAAAAAT CAATAGCATCAA A/A/gap/CTGGTC TAACGTAGCACC TAGATT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4873	cg44002548	1707	ACCGGAATTTTA TATTAAGGGG C/C/A/JTCCTTTT AAATATATGCCG TGTA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17

4874	cg43968302	179	AGCAGGAACCTC CTCACCCACCC TTG/gapJGGGCC TGCCTGAGTCAT TCTCCGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	3.8E-124	17
4875	cg43968302	382	AAACAATTGCC CAGGATAGTGT A/A/CJACAGCTG GAAATTGCTGCT AGAGGA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	3.8E-124	17
4876	cg43303925	1244	TTGGTTACAAGA TCCAGACTTGGG C/C/TJGAGCGGT CCCCAGCCCTCT TCATGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40851 SIRTUIN TYPE 3 - HOMO SAPIENS (HUMAN), 399 aa.	4.4E-124	11
4877	cg43920467	661	AGAGAAAGCCATG AGTTTCCACCAG C/A/GJGACAGT GAGTCCTGAGCA CAACAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa.	4.9E-124	
4878	cg43920467	779	AAAGAAAGAGAG AGAGAGAGAGA G/A/CJGAGAGAG ACAGAGAGACAG AGAGACA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa.	4.9E-124	
4879	cg43927337	992	GCAAGATGAATG GGAAAGAAAATA TTT/gapJAGCTTAA GATCTGTTTGCA AATGGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4880	cg43927337	1300	TGCACTGAGTCA GCTCAAGTGTGC C/A/gapJAAAAAA AAAAAAAAAAAA CAAAACAC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14

4881	cg43927337	1318	GTGTGCCAAAAA AAAAAAAAAAAA A[A/gap]CAAAACA CCAACAACAAAC AAACAAA	A	gap					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4882	cg43927337	830	TGGGAAGCAAGT GGTCTGAGGGC TC[A/G]GCTGGG ACTGGGAGGGA AAGGGCTA	A	G					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4883	cg43948130	519	TTGTGGTTTTTG TTTTTAAAAAAA [A/gap]GGCCCCC AGGGCAAGTTAT TTACAG	A	gap					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5 (PRE-MRNA SPLICING FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa.	2.4E-123	14
4884	cg43948130	519	TGTGGTTTTTGT TTTTTAAAAAAA [gap/A]GGCCCCC AGGGCAAGTTAT TTACAG	gap	A					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5 (PRE-MRNA SPLICING FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa.	2.4E-123	14
4885	cg44026811	296	GAGAACAGTTTC ACAATAAATAAT C[G/A]CTTCTCTA AACTGTACAAA TCCTA	G	A					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03229 ENDOTHELIN 3 PRECURSOR, PLACENTAL SUBTYPE (ET-3) - HOMO SAPIENS (HUMAN), 224 aa.	2.7E-123 (20q13.2 )	20
4886	cg44003626	138	GGCCTCCAGCTA TGGGGTCCAGG GT[C/T]TGAACCT CAGGGCTGGC AGCTTCA	C	T					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.7E-123	
4887	cg44003626	690	CATCTCAGCCTC TCATCCAGCTGA G[G/gap]CTCTGG CCACACCGTGCA AGTGGCT	G	gap					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.7E-123	



4888	cg43271722	241	CAGCTGGGGAG GCCCCGGCTTGT TC[C/A]GACCAAG ATTCCCGGAAGC ACCAGC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O60795 DNA SEQUENCE FROM COSMID 398G5 FROM A REGION OF THE TIP OF THE SHORT ARM OF CHROMOSOME 16, SPANNING 2MB OF 16P13.3. CONTAINS RAR (RAS LIKE GTPASE) LIKE - HOMO SAPIENS (HUMAN), 236 aa (fragment).	3.1E-123	
4889	cg43973009	961	ACAAATGAATCT GTGGATGCATCA A[C/G]CTATCGTC AGTCAAACCCCT TTAAA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P19075 TUMOR- ASSOCIATED ANTIGEN CO-029 - Homo sapiens (Human), 237 aa.	3.4E-123	12
4890	cg44028574	2334	TCGGAACCATCA GCAGAGCCCCA GG[C/G]AGAGTC CTCACCTAAGGG GCTGGTG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4E-122	20
4891	cg44028574	939	CAAAAGTCATGA GTCCCTGGCTTG G[C/gap]CCCACC ACCTGGTGACTC CCGTCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4E-122	20
4892	cg43986720	1022	TCTTCGCCGGGA CATCTGCCAGTG G[C/T]CTCCTGG GCAACTCAGAAG CAGGTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4893	cg43986720	1723	GTGCTGGGTAC CCGCCCGGGAA TG[C/gap]TTCCG CCGGAGTCTCG CCCTCCGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)

4894	cg43986720	1740	CGGGAATGCTTC CGCCGGAGTCT CG[C/gap]CCTCC GGACCCAAAGTG CTCTGGGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4895	cg43986720	45	AATTAAATCTTT AATACAAAATGC[ T/gap]TTTTTTTT TTTAAGATATATC TGT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4896	cg43986720	540	TCAGGGAGAGA GAGATTGGAAC ATTA/GJAATTTTA TATACAAAACC GGTACA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4897	cg43986720	57	TAATACAAAATG CTTTTTTTTTTTT[ T/gap]AAGATATA TCTGTATTTCTTT GTCG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4898	cg43986720	657	ATACTGAAAAA AACCCCTACTCTT TATATATAAATTA ACTGTTTTAATTT CTA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)

4899	cg43986720	658	TACTGAAAAAA ACCTACTCTTT AATTTTAAATTA ACTGTTTAAATT CTAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4900	cg43114691	2497	GATCTGTGTGTC TTTTTTCAGAAAC [G]ATCTGTGACA GGCCCATCAATT TTGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13109 MELANOMA UBIQUITOUS MUTATED PROTEIN - HOMO SAPIENS (HUMAN), 438 aa (fragment).	8E-121	19
4901	cg43932788	602	AACAGCTAGATC AATTTTAGAGAT G[G]gap]CCTAAT AGGCTGGGAA ACAAGTTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75940 30KDA SPLICING FACTOR - HOMO SAPIENS (HUMAN), 238 aa.	8.4E-121	10
4902	cg43958446	375	ATGGAGAGCTCC TCAGCAGCGG CC[G]A]GGGAGA AGTCAGCCAC AGCGGGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43089 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa.	3.1E-120	
4903	cg43923128	2111	TCAAAATTCAG ATATTTTTTTTTT T[gap]GTTCCCT TCTACATAAAA CCTCA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
4904	cg43923128	2825	ACATCTTTTCTTC TGGGCAATAGTA [G]gap]GCCTGGT CTGAAGTCTTAG GTCAAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
4905	cg43923128	2826	CATCTTTTCTTCT GGGCAATAGTAG [G]gap]CCTGGTC TGAAGTCTTAGG TCAATT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1

4906	cg43933691	1085	CTGGGCATCTCT TCTGAGTCTTCT TTC/TCGCATTCA TTTTGGATGTTA ACTTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
4907	cg43004093	527	GCTGGGCCAGC TAACCCCTCTGTG TC[G/C]CCTTGG GCAAACAGCCTT CCGGCCG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	6.6E-120	
4908	cg43004093	564	CAGCCTTCGGCG CGCCGGTTTCATT A[G/T]CGTGAAGA TGTTGGAGCGCC GCTTG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	6.6E-120	
4909	cg43963595	1291	TAGAAAGTGCC GTGGAGCCGGC AG[G/gap]AGGCC CCGCCCGCGCT AGAGAACCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
4910	cg43963595	1441	GGCGGACTCC GCAACGCGTTCC TA[T/C]GTACACC ACCTCCCCCTTCG GCCCTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
4911	cg43937103	1465	TTAATGTGACAG TTTTAAAGGATTT IACJAGTAGGGA ATCAGAGTCCTT TGCAG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment).	1.1E-119	15
4912	cg43937103	1527	CGACTCAATAAC CTCATTTGTTTCT IAGJAAACATTTT CTTTGATAAAGT GCCT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment).	1.1E-119	15

4913	cg43936370	957	CTGTTGTGGAGA AGGTGGCGTTTC C[A/C]CCTTTTCC ATAATAAAATAG AAATG	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:043672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment).	1.1E-119	
4914	cg43936370	806	TGTGCGGCCAAT GATGGATTGT TTC/TJTTTTATGTT TTAAATAAGGAT TTAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:043672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment).	1.1E-119	
4915	cg43950398	898	AACAAAATGAAA CAGATCTCTCCT T[G/T]TACATAAA ACAGCTAAAAAT TTGGC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:075545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
4916	cg43950398	966	TCATGTATTGG CTTGAAAAAAA A[gap/A]JCAACAA CAAAACAAACAG TTACAAG	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:075545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
4917	cg43972658	163	GGCAGACTCCAT GTGTGTCAAACG QT/CJGTGCATGA ATCAGGTTTTTA GAAGG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.8E-119	
4918	cg43972658	450	AAGAAATTTGAT TCITTCCTTTGAT [T/A]CTCTTGGGA AAGAACACATTT CCCA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.8E-119	
4919	cg44002087	1031	AAGAGACCACCA GCAGTGACACCT G[G/C]CAATGAC AGATGCAAGCCC AACACC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:060712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa.	2.9E-119	

4920	cg43256968	728	TACTGAATACAT TGGTCCCTTAGA C[A/G]GCATCAAC AAGCATATTTTA AGAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O60648 HYPOTHETICAL 23.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 217 aa (fragment).	3.7E-119	13
4921	cg29350504	200	ATAGTTCATGAG TCAAAATTTCAAAT [T/gap]AAATGAAT GACATAATATAT AAAAAT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.7E-119	4 (4q21.1)
4922	cg29350504	251	AAATAAAGGGAC AAAGTTCATTTT [T/gap]CCATATAA ACTCATTCAAAC ATACT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.7E-119	4 (4q21.1)
4923	cg43040359	557	CAATAATTTATAT AAATTATTTCTT T[C]CCAAACTAG ATATTTAATAATC CAC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45737 HYPOTHETICAL 83.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 745 aa (fragment).	6.6E-119	
4924	cg43271520	219	TGCAGACATGCT GTCACTGCTCCA C[A/G]CATCAACG CTGGCAGTCCTT GGGGC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to REMBL-ACC:G339409 T-CELL RECEPTOR GAMMA CHAIN VJCI-3(CII)- CIII REGION - HOMO SAPIENS (HUMAN), 318 aa (fragment).	7.6E-119	7 (7p15)
4925	cg43302689	490	GGGAAGCAGGG GATGGGGGAGG TAG[G/gap]CCAG GCCCGCTGGC TCAGGAGCTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34087 CGI-92 PROTEIN - HOMO SAPIENS (HUMAN), 265 aa.	8.5E-119	9
4926	cg44008583	1906	AGAGTAGTTGAA ATCTTTAGGAAT G[A/T]ACTTCTGA GGCCCAAAAAAT GTGAC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15041 HYPOTHETICAL PROTEIN KIAA0069 (HA1508) - Homo sapiens (Human), 226 aa (fragment).	9.7E-119	

4927	cg43067745	135	AATGGATTCTAT TCTGACCAATAC A/C/GJACAGAAA GAGATCACAGAC TCCCTA	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4928	cg43067745	145	ATTCTGACCAAT ACACACAGAAAG A/G/AJATCACAGA CTCCCTACCTTA GAAGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4929	cg43067745	150	GACCAATACACA CAGAAAGAGATC A/C/TJAGACTCCC TACCTTAGAAGA AGGGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4930	cg43067745	78	TATTGCATTGAA AGGTCATTGCAG T/G/CJAAAAGGTTG GGGATTGCTTGC TGCTA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4931	cg43108465	1231	TATTTCCACATC ACATCACAGTTC C/C/TJAAAACGAC TTTAAAGTCTCA AAATT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa.	4.8E-117	1
4932	cg43108465	756	TGTGATTGAATT AGTGCATGGTAA T/G/gap]CATGGC ATATACATTGCTT AAGGTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa.	4.8E-117	1
4933	cg43919033	1057	CATATGTGGACA CCCTCCTGTCCC C/T/gap]GGCCCC TTTCCITTTACCC CAGATT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)

4934	cg43919033	124	CGCCATCTCTGC AGAAGAACTCCT G[Agap]GCCACA CACAGAAGGAAA GTTGATC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4935	cg43919033	894	TGCTATGAAACA TGCGAAAAGTGA TTT/AJTTTCATGGT TTAATTGTGGAT TTTAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4936	cg43919033	895	GCTATGAAACAT GTGAAAAGTGAT TTT/AJTCATGGTT TAATTGTGGATT TTATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4937	cg43919033	896	CTATGAAACATG TGAAAAGTGATT TTT/AJCATGGTTT AATTGTGGATT TATTA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4938	cg42893815	1119	TTAATAAAGAA GTGGTGTTGTTTT TTA/CJCCGTGGC CAGATTTTAAAG AACTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45360 APOBEC 2 PROTEIN - HOMO SAPIENS (HUMAN), 224 aa.	8.6E-117	14
4939	cg43934644	131	CAGGTGACGCTC GCTCCGCTCGTC C[C/gap]GCTCGT CATGGCCTACCC GGGATAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28676 GRANCALCIN - Homo sapiens (Human), 217 aa.	1E-116	2
4940	cg43935587	2560	CGGTAAGGCTAT CATTCAAGACTC TTT/AJGGCTGGTA ATAATATTCAGG TTTAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14141 SEPTIN 2 HOMOLOG - Homo sapiens (Human), 424 aa (fragment).	1.3E-116	X



4941	cg43926002	1227	AGATGCCATCCT CTTTCTCTTTCT [AC]GTTTGCTCA TACTACATTGAG TAGA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4942	cg43926002	1321	TCCTAAAAGCAA AATAAAAACATATT [C/T]GAATGAAAA GACAAGAAAAATC AGGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4943	cg43926002	1449	TCCTTTATTATTA TTTTTTTTTTTTTT gap[GAAAAAAGC TCATTTTCATGCT CTGC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4944	cg43926002	2097	GACACACTATCA TAGTTAACATAG TTT/gapJAAGTTCA GCACCTTGTCCTCA TTTTAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4945	cg43926002	2302	TTGTCCTTCAAA CTCCAAGGTTCC C[C/T]TGTTGGCC CTCTCCCTTACC CTGGGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4946	cg43926002	2402	ATAATTTAACTAC CCTTAATTACTTT gap/AJAAAAAAA AAAAAAAAGCCTT ATGAT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4947	cg43926002	2417	CTTAATTACTTAA AAAAAAAATAAA A/gapJGCTTTATG ATTTTCATAACTT ATTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10

4948	cg43926002	2417	TTAATTACTTAAA AAAAAAAAAAAAA gap/AJGCTTTATG ATTTTCATAACTT ATTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4949	cg42545645	214	TTTCAACAAAAG AATTTTCTAAGC A/CJTJGCTGCTG TTACCAGACACT TGAGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa.	1.6E-116	
4950	cg42545645	394	ATCTTTTATGAAC TGCGAATTTGGG gap/GJTCCTGCAA TGGCACTGGTAA GTGAC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa.	1.6E-116	
4951	cg43993887	770	AAGCATCTGAA CTTTTAATGAAC T/GJTGAAGGACA ACAGCATCTTCC CAAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75934 PUTATIVE SPLICEOSOME ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 225 aa.	3.4E-116	1
4952	cg43932292	3000	TAAATTTTTTG GTCCTTTTGTAA A/GJAGAGTGTGC TGCTGTAAGAAA TCTC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15631 TRANSLIN - Homo sapiens (Human), 228 aa.	4.3E-116	2
4953	cg43921057	221	AGCCAATATAGT TTCTTCTCCATA T/AJTAACATAAA CAGCTACAAGAA CCCT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-116	12
4954	cg43921057	84	AACTAAAAACAA TTAGATGTTTCAG A/GAJGCAGTGTA CAATGAACGAGA AATCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-116	12

4955	cg43258389	707	GAGGGTAACTCT GCTGGACATTCC A[A/C]TTCACTCA TCTGCGTGTCCC CCACA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SP TREMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa.	1.6E-115	5
4956	cg42832298	51	ATAACCTTTATTT AAAATAGATTAT A[C/TTTAGGAAA GCTCATTTTATAT GAG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SP TREMBL-ACC:O75446 MSIN3A ASSOCIATED POLYPEPTIDE P30 - HOMO SAPIENS (HUMAN), 220 aa.	2.4E-115	4
4957	cg43307713	101	CTGGCCCCGTCAC CGGCCGCTGAA GG[C/gap]AGCAC TGCTGGGCAAG GAGAAACAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4958	cg43307713	141	AGGAGAAACAAG GCCACACCTGCA A[C/A]CTGGGCT GCAGGGTGAGG TGCTCC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4959	cg43307713	33	TTTTTTTTTTTT TTTTTACCAA T/AJTGCCTTTTAT TTACATACGAGA AAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4960	cg43951899	221	CCCTCCAGTTT GGGGTCTAAAC C[G/A]AACAGGA GAGGTGCAGGG GACCAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4961	cg43951899	307	GCAAGGGGTCC CAGGGCCTGGA GCC[C/gap]GAGG CCCAGCCAAAG CACACAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9

4962	cg43951899	369	TTTATAGTGGGAA GCTCCAGGCCCT G[C/gap]CCCTCC CCGGGGGCCTC GAGGTCGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4963	cg43951899	372	TAGTGGGAAGCT CCAGGCCCTGC CC[C/gap]TCCCC GGGGGCCTCGA GGTCGGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4964	cg4398647	1269	TCTTTTCTCAG GCCTGAGGGGG AA[C/gap]CATTTT TGGTGTGATAA TACCCTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34072 CGI-78 PROTEIN - HOMO SAPIENS (HUMAN), 251 aa.	3.8E-114	1
4965	cg4399521	1329	CTTCTGATTGAG CGGTGCCATGG C[C/]GGTCTCC GTGGGCGCAGGG TTGGGCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	
4966	cg43982971	1328	AGCCAGGTGTCT TCCCGGGCCCT GC[C/gap]AGACC CTGCTCACATTG CCTCTGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4967	cg43982971	1529	GGCTTGGGTGG CGTCGGGGCAG GG[C/gap]GCCG AGGCTGGGAGG AAGCCCTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4968	cg43982971	1680	GGTGGCTGCTG GGTGGGGCCGG GAA[C/A]AAGGG CCCCTGACCCCTG TGTGCTGG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	

4969	cg43982971	1773	AGCTTTGTGCCC CTGGATGCGCTA A/C/AJATCACTC TTGTTTGTCCCT GGACT	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:P97765 VWV-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4970	cg43948724	2006	TGTGAACCTACC TGCCTTGGAGAG G/G/gap/CCCAGG TCCCAAATCTCT TCAAATT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4971	cg43948724	2109	TCAGTTTATGC CCCATTTGGATTA C/gap/TTTTTTTT TTTTTTTTTTTT ACTCT	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4972	cg43948724	2159	TTGAAAGCTTTG TTTTGTGTAGT C/gap/G/CTTTTG GGAAGAATCCAG TATTATC	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4973	cg43948724	2347	GAAATGCTGTTA GTAAATTTCTGT G/gap/C/JATTTTTT TTTTTAATTTGT TTTGC	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4974	cg43948724	603	GCATCAGACCTG CATTGAACAGTC C/G/JGTGGAAA GGCCAAGCAGT GACCAGG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)

4975	cg43946376	139	AGCGATATAATT TAAAGTTTTTTT [gap]/TCATTAGAA ATAAATGTATAAA AATA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4976	cg43946376	341	ATTCACCAGGAT ACGACTGTTGGA C/C/AJAGCTGCT GGAGATGGACCT GCTACC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4977	cg43946376	391	CCCTCAGCAGCC TCCCCACCACAA G/A/GICAAGTGAT CTCAATGTCGCC AAACC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4978	cg43946376	832	AATGTATAAACA TTCTCTGAAACC A/T/C/JAGCAGCCA TAAACAGTGCTG GTCAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4979	cg43983566	265	TACAGACAAAT TGGCTTTTATCC C/T/C/JTTTGATAC CAATATATGTGT ATACA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:060487 EPIHELIAL V-LIKE ANTIGEN PRECURSOR - HOMO SAPIENS (HUMAN), 215 aa.	3.2E-113	11

4980	cg43971133	1167	TTGTTATATAGT GCTGACTTTTTT [G/T]TTTGAAT AAACAGATTGGT AACC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4981	cg43971133	125	CCCCACGCGGA AGGCAACTGCCT GA[G/A]AGCGC GGCGTCGCACC GCCCAGAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4982	cg43971133	40	GCCGGCTGCCC GCCCAGTTGTTA CT[C/T]AGGTGC GCTAGCCTGCG GAGCCCGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4983	cg43971133	87	CCGTCCGTGCTG TTCGCGGCAAG G[C/gap]CTTCC CAGTGTCCCCAC GCGGAAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4984	cg43257585	161	CCGCCCCACCCT GCGCGCTCCTC CGC[gap]/GJCGGG GAAGAACCTGCG CGGCAGGAC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60682 ACTIVATED B CELL FACTOR-1 - HOMO SAPIENS (HUMAN), 218 aa.	1.8E-112	
4985	cg43934153	159	ATGTCCAGGAAG AAAAAGATTAC A[T/G]GCTGCTC GCAGTAAGTAGG AGCTTT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBL-ACC:AA42945 RING1 INTERACTOR RYBP - MUS MUSCULUS (MOUSE), 226 aa.	2.8E-112	3

4986	cg43916671	898	TGAAGGCAGAAG CCCACCATGCAG A[G/gap]CTGTGA ATCTAGAGGCTC TGAGCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99470 SDF2 - HOMO SAPIENS (HUMAN), 211 aa.	5.9E-112	
4987	cg42890336	1181	ATAATAAATGCA ATTATAAACTATA [A/T]AAAAGAGGG TGCAGAGGAGG GAATG	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa.	1.2E-111	
4988	cg43980619	386	TTCAATCCGTCT GTTAAGGGCAG GG[C/gap]CGGGC TAGTGGCAGGA GAAGGTCAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q00501 TRANSMEMBRANE PROTEIN DELETED IN VCFS - HOMO SAPIENS (HUMAN), 218 aa.	2.1E-111	22
4989	cg43942219	944	GCGAGCGCGAC GCACGGCTGGC CAG[C/T]GACCCCT GCTTCAGCCCCGA CCTCAAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4990	cg43942219	178	GAATCCACTGGC GAAAGATGCCTT TTC/TTTAGGAAGC AGAGCTCCCTGA CTGGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4991	cg43942219	184	ACTGGCGAAAGA TGCCTTTCTAGG A[A/G]GCAGAGC TCCCTGACTGGG CTAAGA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4992	cg43942219	190	GAAAGATGCCTT TCTAGGAAGCAG A[G/gap]CTCCCT GACTGGGCTAAG ATAGTTC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2



4993	cg43942219	208	AAGCAGAGCTCC CTGACTGGGCTA A/G/AJATAGTTCA GATTGATCTTAG GTCAA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4994	cg43942219	217	TCCCTGACTGGG CTAAGATAGTTC A/G/AJATTGATCT TAGGTCAATGGT AAGAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4995	cg43942219	48	TTTTTTTTTTTT TTTTTTTTTAAAJA /G/GAAAAAGTGT TTATTATAGGCA ACA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4996	cg43942219	49	TTTTTTTTTTTT TTTTTTTTTAAAJA G/AJAAAAAGTGT TTATTATAGGCA ACAA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4997	cg43942219	54	TTTTTTTTTTTT TAAAAAGAAAAA gap/AJGTGTTTAT TATAGGCAACAA CACCA	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4998	cg43957889	1187	GATATGGGAAGC TTCTGTGAGTGC A/G/TAAGGATGG GGGCTGGAGTC ATTGTTA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
4999	cg43957889	1551	ATTACAGGTGTG CACCACCACGCC T/G/AJACTAATTT TGTATTTTGTAGTA GAGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12

5000	cg43957889	203	AGGCGCAGAGT ATTGGGTTTGGC TG[ <i>gap</i> ]CCTCG ATTTAAAGAGAC AGAAGCTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:000577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
5001	cg43957781	60	CTGTTTACTTCA CTAAACCTGGA G[C/T]GAGGCAG GGAAAAGGTACA TCAATG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075790 SEVEN TRANSMEMBRANE DOMAIN PROTEIN HOMO SAPIENS (HUMAN), 224 aa.	3.2E-111	19
5002	cg43960639	359	TGCATCATGAAA CAGAGGCAGGG CC[C/ <i>gap</i> ]TAAAGC TGCCCAAGAGG CCTGGGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa.	9E-111	
5003	cg43036790	37	GACCAAGCTGTC TTGTTTTGCGTA C[A/G]TCAACACT ATGCTGCTTCCA ATATT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
5004	cg43036790	68	ACTATGCTGCTT CCAATATTCCCTA G[C/T]CATTCCAC AGGTAATGATTT TTCAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:075058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
5005	cg4396282	846	ACCTCCCCAGAC AGGCATTCCGAG T[G/C]GGAGGCG GGAGCACGTAC CGCAGGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12
5006	cg4396282	880	GAGCACGTACC GCAGGCGGAGC TAG[G/C]GAGGT CTAGATGGAGG GAGGGTCCA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12

5007	cg43950821	807	AGAGCGCGCTC ATAAAGGCAGCT GA[gap]GGGGC ACCTGCCACCCC ACTGATGC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	3.7E-110	
5008	cg43950821	811	CGCGCTCATAAA GGCAGCTGAGG GG[gap]CACCT GCCACCCCACTG ATGCCCAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	3.7E-110	
5009	cg43325007	537	AATCAGTGTTTT ACTTCAGCAAAC G/GAACCCCTGG GATAACACCCAGT TGGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.8E-110	20
5010	cg43116651	791	TGGCAAGAAAAT GGACCCACCTTT C/C/TGCACAGG ACCGGAGGCAA AGTCGT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa.	1.6E-109	2
5011	cg43956410	189	TCCTTTCAGTTG CTGGGAGCGGT GA[G/gap]GCCCA GCCCTTTCCCT TCCTCCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5012	cg43956410	256	GGGGCCTGGCA GGGGTGAGTG ATG[T/gap]GATC TAAGGGTCCCTG GAGAAGGGT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5013	cg43956410	348	GAGGTCTCAGG GCAAAGGGAAA GGT[G/T]TTTGA TGAAGACTGAGG CAGTGCC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1

5014	cg43956410	366	GAAAGGTGTTTG GATGAAGACTGA G[G/gap]CAGTGC CTACCTCCCTCC ACATCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5015	cg43928772	164	TCCAGAACTAT CTTAGATGAAAT A[T/A]TTGAAGAA TTCAGTTAAATAT TTAT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5016	cg43928772	329	TCCAAAGGCAG AACTTGAGCCAA G[C/G]GATAAATA TAAGCAACCAAT GGCT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5017	cg43928772	500	GTCTTAAATAAG TTGCATTTTCAT G[G/gap]CAAGCC CTCCACTGCCAG CAATGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5018	cg43327495	160	TCAAGAAGAGGA AGAAAAGGCTCT G[C/gap]CTTATA CCATAAAATCA AGTACTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
5019	cg43327495	161	CAAGAAGAGGAA GAAAAGGCTCTG C[C/gap]TTATAC CATAAAATCAA GTACTCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
5020	cg43327495	229	GCAGGATATTG TTTCTCCAGTTT T[C]TGGCTCTAA GAAATTACACTT TCAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17

5021	cg43942004	1769	CCGTGGTCAGA GTGCCACTGCG GGA[G/gap]CTCT GTATGGTCAGGA TGTAGGGGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5022	cg43942004	1932	AGTGTCTCCCCG TGTCCTCTCCCT G[C/T]CAAGTCTC AGAAGAGGTTGG GCTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5023	cg43942004	2003	TCCCTCACCCCC ATGGCCCCAGG CC[C/gap]ACAGC GTGGGAATCACC TTTCCCTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5024	cg43942004	2260	CACCCACCTCAC CAAAACGATGAA G[G/T]TATGCTGT CATGGTCCTTTC TGGAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5025	cg43976960	966	GCTCTCCTTTGC TTGTCCCTCTTG C[C/gap]TTCGGT AATATGTATAAA CTTACAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5026	cg43976960	1076	GTTTGTAGTTTGA TAATAAATCTT[ T/gap]GGAACTTT AAAAAGATCTAG TCTGT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)

5027	cg43976960	1087	GATAATAAATCT TTGGAACCTTTAA ATJAAGATCTAG TCTGTTACACCA TTTA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5028	cg43976960	1221	ACATTATTATTT TTCATTGTGAGA C/TACTAAAACT GTTAATCAGACT ACA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5029	cg43976960	2103	AAATTTAAAACT GGCCTGGTTTGC Ggap/TTTTTTA TCAAGAGAGCTT AACAGA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5030	cg43976960	2109	AAACTGGCCTG GTTTGCCTTTT Ggap/TJATCAAGA GAGCTTAACAGA TAAAAA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5031	cg43979124	187	CAAGTTGCTGT ACAATACTGAGA A/C/ATTTTCATGA AAACGGTATTTA ACAAT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.1E-107	
5032	cg43979124	838	AATACAGTAAAT TCCAGGTGCCAC C/AGAGCTTCAG AGACCACAAGTT TCAAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.1E-107	
5033	cg43997460	2887	AGCCCGAAAGAA TCTCTTGCTGCT G[C/gap]AAAGAA CAGATTTTATAT TCTTCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O18147 T27E9.4 - CAENORHABDITIS ELEGANS, 625 aa.	3.5E-107	3

5034	cg43997460	4010	GACATTGTACTC AGTGGGCTTG GG[ <i>gap</i> ]CCTAG CCCAGCTCTGAG CAGAGGAC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O18147 T27E9.4 - CAENORHABDITIS ELEGANS, 625 aa.	3.5E-107	3
5035	cg43933543	205	TAAGGGTTGGGT CTCCTGATGAAC TTCATTAAGTACC CAGTAAGCTCTT CTCTT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa.	3.5E-107	6
5036	cg43933543	45	TTTTTTTTTTTT TTTTTTTTTACA CTATCTGCAGC AGATTTTATTAG ATG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa.	3.5E-107	6
5037	cg43948067	1147	TCCTCTGTTTAA GTTAGATCACTT CTATTTCTCAG GTAATGACTTTA TTTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5038	cg43948067	1148	CTTCTGTTAAG TTAGATCACTTC ATATTTCTCAGG TAATGACTTTATT TTTT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5039	cg43948067	1149	TTCTGTTAAGTTT AGATCACTTCATT TATCTCAGGTA ATGACTTTATTTT TTT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5040	cg43948067	1150	TCTGTTAAGTTA GATCACTTCATT TATCTCAGGTA TGACTTTATTTT TTC	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20

5041	cg43948067	1413	GGTTTATAGCAT AGTAAGGTATTT TTAG/CACAAAAT ATATTTTAAACT ACAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5042	cg43948067	1614	CCTTAAGGAGAC TGAATATCAATA C/C/gapJAGTTTC CAAGGAGTCTT GTTGAAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5043	cg43948067	1789	TTATCAAAAAAAA AAAAAAA A/gapJCTACCCAA AATATAGTTGTAT TTTT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5044	cg43948067	65	TTTATTAAACAAA GTTTTCCCTTAAT T/C/CACATTTCAA CTTTATTAAATAG TC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5045	cg43260407	446	TGCTGCTGTTTA CACAAGTCCAGA C/GA/ICTGCCAG GGCCTGTTGGG ATCAGCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa.	5.6E-107	14
5046	cg43260407	479	GGCCTGTTGGG ATCAGCTCAGTC TG/C/TGACTAAA ACAGCTGGATCA TCGACT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa.	5.6E-107	14
5047	cg43967668	789	GGTAGGCCCCC CAGAGCTCCATG CT/C/GJGTGCGC GGCGGGGGCT GCTGCTGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107 3 (3p22)	



5048	cg43967668	790	GTAGGCCCCC AGAGCTCCATGC TC[G/C]TGC GCG GGCGGGGGCTG CTGCTGCC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRANECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
5049	cg43967668	845	GCGGGTCTGGG TCCGAACGCAGT GA[G/gap]CAGCC ACGGCCCCAGGC TGCACGTCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRANECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
5050	cg43297716	3201	GGCTGGCTGCATG TCCCCCAGGATG G[G/gap]CTTCGA GAAAGACAACT TGCTCTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPL) - Homo sapiens (Human), 202 aa.	1.2E-106	22 (22q12.1)
5051	cg43297716	3952	AGCACATGGCCTT TGGGTGACAAAT TT[C/C]CTCTTTGA TGAATGTACCCCT GTGGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPL) - Homo sapiens (Human), 202 aa.	1.2E-106	22 (22q12.1)
5052	cg43297716	992	GGGGCCCTGTC CAAGGGTGGCT GGG[G/gap]CCCA GGGCATCGCTAA ACCCAAATG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPL) - Homo sapiens (Human), 202 aa.	1.2E-106	22 (22q12.1)

5053	cg43269003	1190	CAAAAGGATAAA AATGTGAACGAA GTTgapJTAAACAT TCTGACTTGATA AAGCTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34784 HYPOTHETICAL 127.9 KD PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 1181 aa.	1.2E-106	
5054	cg43924804	89	GCGCAGGAGGA GGAGGAGGCCG TGG[G]gapJCGAC GGCGATGGCGA CGGGGACGCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O48696 F3I6.23 PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 525 aa.	5E-106	6
5055	cg43982339	1043	ACAGTGGCAAAA ATGAAAAA A[gap/A]TAAAAAT TATAAAAGAGGC AAAAAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5056	cg43982339	1043	ACAGTGGCAAAA ATGAAAAA A[gap/A]TAAAAAT TATAAAAGAGGC AAAAAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5057	cg43982339	1087	AAAAAAGACAC ACTATTCTCTGC C[gap/C]TCTAAA ACACAAATTAAT AAAAGAA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5058	cg43982339	153	AACATCTCCCAT CTCTCTGGATT CTT[C]TTTTCCTT CATTATTCCTGC TAACC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)

5059	cg43995374	110	AAGATACGAGAT C CCCGCTGCCCTTG GTC/gap/AAATTCT GTTATCAGAAAG ATAGTGA	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5060	cg43995374	22	AGGAATAGAAAA A TTTTTTGTA[A/G] TATGGAAGTTGT AAAGCTGTGTTT T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5061	cg43995374	384	CCCCAGCCCATGCC gap CTCTCCCCACCA C[gap/A]AGCACC CCGCCTGACCCT AGTGTCC	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5062	cg43995374	385	CCCAGCCCATGCC gap TCTCCCCACCCAC A[gap/A]GCACCC CGCCTGACCCTA GTGTCCA	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5063	cg43995374	385	CCCAGCCCATGCC gap TCTCCCCACCCAC A[gap/A]GCACCC CGCCTGACCCTA GTGTCCA	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11

5064	cg43995374	385	CCCAGCCATGCC TCTCCGCACAC A[gap/A]GCACCC CGCCTGACCCCTA GTGTCCA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5065	cg43995374	741	AGGAAGAAATGG AAATATCTGTGC A[gap/G]GGCCCA AGCCCGGCCTG GTGCGGGA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5066	cg44005345	2155	CAGCTGAAATTT GTTTCATAGCTG TTT/C[GGTCACCC AGTTCTAGCCAA CCAGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5067	cg44005345	2837	GGTCACACTCAT CTGGTAGTGCAT G[G/gap]CGACGC GCTCCCGGTGCT GAAAGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5068	cg44005345	417	CAGCCTTCCAGG TCCTCAACTCCC G[C/T]GGACGCT GAACAATGGCCT CCATGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5069	cg43988395	981	TGCAGCAAGTGC CCAGCAGAGCT GC[T/C]GCGCTAT CTGGCATTCTG CGAGGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60443 ICERE-1 - HOMO SAPIENS (HUMAN), 234 aa.	1.5E-104	7

5070	cg44912062	810	GGACCGCTGTG GACCTCGGAC CTG[G/gap]ACGC CGTCTGGCTGC GCAGGAGGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
5071	cg44912062	836	ACGCCGTCCTG GCTGCGCAGGA GGG[G/gap]CCGC TGGCATGGACTA AGAAATCCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
5072	cg43963123	1068	GCCAGGTGCCT GCATCTCACTGG TG[C/T]GGCCGT GGCACCTGAGG GAGCCAC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5073	cg43963123	343	TCCTTTTTTTTT TTTTTTTTTTTTT// GJTAAAGAACAA AAAGCTTTACTC GT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5074	cg43963123	346	TTTTTTTTTTTT TTTTTTTTTTTTT// GJTAAGAACA GCTTTACTCGTG CT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5075	cg43963123	449	CCCTCCATGGAA GGCACCCAGGCG GG[G/C]AGGTGG GTCTGCTGGGAT GGGCAGG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5076	cg43963123	739	CGGCGTCCCCC ACAAAGCCTGCC AG[G/gap]CTGAG CCCTTGCAATGG CCGTGGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17

5077	cg43963123	941	CTGGGTGCGGG GGAGGGGCACT GCG[G/gap]CCCT GGCCATCAGCCT GGCTGTCTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5078	cg43988007	1549	AGGTAGTTTTTA GTGGTTTGGGT TTC[G]TGTGTGTG TGCAATGCCCTGTG CTTTT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment).	3.6E-103	5
5079	cg43988007	315	AAATTGAGTCCA TCAGCTGTAAAT AIC[gap]AATTTTA TATTTGGCTCAA GTGGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment).	3.6E-103	5
5080	cg43934831	1109	CTCAGTAGCCTG GGGTTGGTGCA GA[G/gap]CGTCC AGAGAGGCAAG GGCATAAAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa.	1.9E-102	5
5081	cg43934831	969	GCAAAACAATTT CTCAGCCAGGA GG[C/gap]TCCAC CTCCCATTTCCT TGTAGACA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa.	1.9E-102	5
5082	cg43972159	894	TGCTTGCCCTTA CCCCAGCAACG CG[G/gap]CGCGG CCAGAACCCAGAA TGCAATAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.6E-102	7 (12q24.1 )
5083	cg41045063	848	GGGTGGGAGTG TGGTGGGGGGT AGT[G/T]TGTGGC AGGACAAGAGAA GGCAITG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa.	3.3E-102	19 (19p13)

5084	cg43943283	390	AATTGAGAGCGT TTTCGCACTCCA G[G]GGCTGCT CCTGGCGGCTCT GCGGCC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa.	1.1E-101	5
5085	cg43966895	149	TTTTTTTTTTTT TTTTTTTTTTTT /TCCATTTCACT GATTTTTATTAG GG	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD42057 NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT - HOMO SAPIENS (HUMAN), 179 aa.	2.3E-101	7
5086	cg43999564	34	AAGCTGAAAATC ACAGGCTGATAG C[C/gap]TCCATTT TAATTAATATTCT ACTAT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15
5087	cg43999564	65	TTTAATTAATATT CTACTATTCACTI T/C]TTTTTTTGGT TTTTAAAGATGG TTT	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15
5088	cg43999564	70	TTAATATTCTACT ATTCACITTTTTI T/AJTGGTTTTTA AAGATGGTTTTA TAT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15

5089	cg43926487	32	CTCTTTTTTTTT TTTTTTTTTTTTTT CJCACGGAACA GCCGTTTTTATT CCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa.	3.8E-101	20
5090	cg43958634	1217	TAGATACAGGCA CCGAGCGTCGA GG[G/gap]CACAG CAGCAGGCCGG CCCTGTTCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5091	cg43958634	1268	GAAGAAGGGTG GTTGAGCTCCTG GC[C/gap]TCCGG ATCTGCAGCCAC TGATGGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5092	cg43958634	227	ATATAAACATA GAATAAACCGCA G[G/gap]AAGAAA TATTGGTCTGGA ATTCCTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5093	cg43958634	315	TATCTCCCCCA CACTGGGGCAG GC[G/A]GCGGAA TAAGCTCCAGCG TTCATGC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5094	cg43958634	341	GCGGAATAAGCT CCAGCGTTCATG C[G/A]CCACTCAC AGGACTGCTTAC CCCCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5095	cg43983699	1819	TTTACTGTTACAA TGTGCAGCCGC C[gap/C]JAGATGG TATCCTCCTATG GAAAAA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10



5096	cg43983699	189	TTGCTAGAGGGA AGGAGCTCCTG GCJAGJTACATC TACTTGGATAGA AGAGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC: AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10
5097	cg43983699	36	TTTTTTTTTTTT TTTTTTTTTTTTTT GJTTCCTTTCATC TTTTTATTGATAG C	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC: AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10
5098	cg43980312	1090	ACACTTAGAAAT CAAAACACGTC ATT/ATCCTTGAGA GCAGACGGCCG TTAGCA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5099	cg43980312	1094	TTAGAAATCAAA CCCACGTCATCC TTT/gapJGAGAGC AGACGGCCGTTA GCAAAGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5100	cg43980312	2161	TTTATCATTAAAGT TGCCAGAAATGGC TTCCTTTAATGA AAACAAAAAACA AAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5101	cg43980312	3050	CGCTCGCTTCCT CCTCCTGCGCCT GTC/gapJTCCCGC CGCCCGCAGCT GCGCCCCCG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)

5102	cg43980312	521	GACTTGGACGG CTCACAGTTTAA AA[C/G]AAAAATTA GTGGTAAATAG AAAAAG	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5103	cg43939240	347	CCTTCCCCCTCCC GGGAGTGGCAG AG[C/gap]CGGGC ACACCACAGGCA GGCCCTCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5104	cg43939240	732	TCTCTTGGCCCC TCCCATTTCCAG A[G/gap]GCTCAA GAGCCCTTTAGG GCAGGGC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5105	cg43939240	733	CTCTTGGCCCCCT CCCATTTCCAGA G[G/gap]CTCAAG AGCCCTTTAGGG CAGGGCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5106	cg43941552	1041	ACAGGGTCAGTG GAAGCCCCAAC GG[G/gap]AAAGG AAACGCCCGG GCAAAGGGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	

5107	cg43941552	1175	GAGGATGGGAG TGGGCAGAGGT GGC[G/A]CCCAG GGCCCCGGGAA CTCCTGCCA	G	A					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	
5108	cg42917153	969	CCCCTTCTATC CTAAACACATCC AT[A/JAAAAAATG TGCTTATCACTG TGCTC	T	A					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P45973 HETEROCHROMATIN PROTEIN 1 HOMOLOG ALPHA (HP1 ALPHA) (ANTIGEN P25) - Homo sapiens (Human), 191 aa.	2.1E-100	12
5109	cg43252708	386	GGGTGGCTTCT GTCCACTTGCTG A[G/T]CAACTTGT TTTCCTTTTCACA GTGG	G	T					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5110	cg43252708	393	CTTCTGTCCACT TGCTGAGCAACT T[G/T]TTTTCCTT TTCACAGTGGAT ATGAC	G	T					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5111	cg43143591	62	TTATTTTATTTA CAACAGAAATTGG T[G]GGCTTTATT CCTCCAATCTTA GGGA	T	G					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99966 MELANOCYTE-SPECIFIC PROTEIN 1 - Homo sapiens (Human), 193 aa.	3.4E-100	
5112	cg43925214	372	CCTCTGCACTCG GGCGGATCGTTA A[C/A]TCCCCAA GTTACAACTGAG TTGCT	C	A					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10
5113	cg43925214	77	TTTTTTTTTTTT TTTTTTTTTTTTTG /TTGGAAACAA CACCTTATTTATT CA	G	T					SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10



5119	cg43941550	372	GCTCCCATTTCT CCAGGGTTTGTG C[C/gap]TGCGGT GTGGGCAGAAG CAGCTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5120	cg43941550	472	TCCCGTTGGG CTTCCACTGACC CT[G/T]CTCACCG GAGGCGTCCTA GATGTAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5121	cg43941550	482	GCTTCCACTGAC CCTGCTCACC GG A[G/gap]GCGTCC TAGATGTAGTAG AGCGGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5122	cg43941550	483	CTTCCACTGACC CTGCTCACC GG G[G/gap]CGTCCT AGATGTAGTAGA GCGGCAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5123	cg43950149	285	ATATCTTGGCTG TATTATTTCTTAC [C/T]GTGAGAAA GAGACTTAGTAT ATGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12

5124	cg44925165	2067	TGCCAACACCAA GCTCTGAGTTAA C[ <i>gap</i> ]/TJGTGCTT TCTTCTCCTGGC CCTGACA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75672 HMGBCG PROTEIN - HOMO SAPIENS (HUMAN), 196 aa (fragment).	7.1E-100	
5125	cg42903839	860	GTAAAGTGAATG TCTAGTATCTTCT [A/G]TTGAGAGTA CTACTATTAATTA AGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6
5126	cg43917034	1156	GAACACTGGCAG TAGAGTGGAGG GG[C/ <i>gap</i> ]/CGAAG CCACATCATCAA GGTGAGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa.	1.5E-99	2
5127	cg43917034	65	TTGAGTGCITTC TAGGTGCCAGG CA[C/ <i>gap</i> ]/AAAGC CAGGCACTGTTA ATACAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa.	1.5E-99	2
5128	cg42646578	127	TAATCAGATGTA ATAAAAACAAAT GT[A]/TTAAAATA CAAAAATGTAAT GTATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	2.4E-99	
5129	cg43968421	663	TCCCCCGCGGA GCTGACTTCAGC AG[C/ <i>gap</i> ]/CCACA GCTGTGGGGCTT CAGCAGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43240 HYPOTHETICAL 85.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 754 aa (fragment).	6.4E-99	1
5130	cg43327570	638	TACTCCTTCAGA GCACTGCTGAAA AT[C]/GGATCAAA CGTGGAGATCCC CCAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75223 WUGSC:H_DJ077023.1 PROTEIN - HOMO SAPIENS (HUMAN), 188 aa.	3.5E-98	7

5131	cg43920704	16	TTTTTTTTTT TT[C]CAAATTA TAGCATTTTATT TTCCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:G1488414 N8 GENE PRODUCT LONG ISOFORM, N8L PROTEIN=D52 HOMOLOG/LEUCINE ZIPPER PROTEIN {ALTERNATIVELY SPLICED, CLONE HK4A1} - HOMO SAPIENS, 248 aa.	1.2E-97	8
5132	cg43925352	1925	GGCCAAAGTAGCT TTTATTCTGGCT G[A]G[C]AGACTG TACTTTTGTACT TTAAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5133	cg43925352	2077	TGGTTAACTTCT CCAAAATAGTGT C[T]A]GGAAGGA GTTTCTTTTCTT CTGTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5134	cg43925352	2196	CGCACTGCGCG CTCCTCTTCTCT CG[C]gap]TCCGC CTGGCGGCTGG CGAAAGTCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5135	cg43925352	2225	CCTGGCGGCTG GCGAAAGTCAGC TC[gap/C]TCCGG GGCCTCATCGTC AAACTCAT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5136	cg43981803	29	TTTTTTTTTTT ACAACAAGCCAA [C/A]ACATATGCT TTATGGTTCTGT TTCA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X
5137	cg43981803	31	TTTTTTTTTTTAC AACAAGCCAA [C/A]ATATGCTTT ATGGTTCTGTTT CAAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X

5138	cg43956754	1327	TTCTATTCTGAAAT AACAAATTTTTT T/gap/GAAGGTCA AGTTTTTCAATG GCACA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40377 PTD014 - HOMO SAPIENS (HUMAN), 187 aa.	1.4E-96	15
5139	cg43974514	1202	TTCTACCAGGGT CCAGGACTAAGG C/GA/JTTTTCTC CATAGCCTCAAC ATTTT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:G545790 DARPP-32=DOPAMINE AND CAMP-REGULATED PHOSPHOPROTEIN - HOMO SAPIENS, 204 aa.	2.8E-96	17
5140	cg43988005	226	TGGGGTCACCTG GCTTCCTGGG GA[C/gap]CCGCA AGAGGGGCAG GGAGCAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13938 CALCYPHOSINE - Homo sapiens (Human), 189 aa.	3.6E-96	
5141	cg43935925	1130	GCGTCCATGGC GGCGCGAGCTG CAG[G/gap]CCAG AGCTCACGGTCT CCTCGGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	16
5142	cg43935925	148	AGAGTCTAAAT CAGCCCAAGAAA TTC/GJAGGATCAA GAAGGGGTAAAA AGCCG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	16
5143	cg43935925	239	TCACTGAACACC TGCCCAAGTGTG ATT/CJGGCTTCCA TGCAGGAGACC CAAGTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	16
5144	cg43925764	443	AATATCAAGACC AATCTAGACTTTT TT/GJTGCTCTTA CATGTGAAATGG ATGT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC72976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa.	7.5E-96	5



5145	cg43925766	911	AAATTCGTGGTT AAAAGCTTCCTA ATCTGGGTAACA GACCATGGGAG AGATAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC: AAC72976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa.	7.5E-96	5
5146	cg42750616	143	GCACCAATGGC TTTGGGCATAAT G[C/gap]CCCTCC TCCATAAGGTCC CTACCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC: Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	1.4E-95	
5147	cg43971745	1252	CAGACAGGAAGA GACCACCCCCC CC[gap]/CjAAAAA AAGAGCCCTGAA GACCTCTG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5148	cg43971745	1252	CAGACAGGAAGA GACCACCCCCC CC[gap]/CjAAAAA AAGAGCCCTGAA GACCTCTG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5149	cg43971745	306	CAGGCAGGAGG CAGTGGGCTGG CAG[C/gap]/CACC CTGGGCACAGAA GAGCAGACG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5150	cg43971745	307	AGGCAGGAGGC AGTGGGCTGGC AGC[C/gap]/ACCC TGGGCACAGAA GAGCAGACGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5151	cg43971745	769	TGGTCTTGGGG GGTTGTCCCCCT CC[T/C]TCTGGCC TTGGAAGACTCT TCCCTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1

5152	cg44924968	43	TTTTTTTTTTTT TTTTTTTTTTTT[G /T]GAAACAAAA TAAATTATTGCT CC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
5153	cg44924968	44	TTTTTTTTTTTT TTTTTTTTTTTT[G G/T]AAACAAAA TAAATTATTGCT CCT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
5154	cg43280516	666	CTTCTGGGACCT GCCGGCCTCCC GG[G/gap]CCAGC TGCCCCACCCCT GCCCATGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.8E-95	19
5155	cg43280516	718	TGCTCTGCACGG CTCTGCTGCTCG G[G/gap]CCCACA GCGCCGTCCCAT CACAAGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.8E-95	19
5156	cg43129980	18	TTTTTTTTTTTT TTTT[A/T]CCTTT CTGAAGAAAAA CTTTTAT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76840 KIAA0996 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa.	6.8E-95	
5157	cg43950632	1046	TTTATGTTATATG TTTACAAGCCTG[ G/A]ACCCCGCGC CTCTCCTGCGG ACGC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
5158	cg43950632	1047	TTATGTTATATG TTACAAGCCTG[ A/C]CCCCGCGCC TCTTCCTGCGGA CGCG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1

5159	cg43984244	1048	TATGTTATATGTT TACAAGCCTGCA [C/A]CCCGCGCC TCCTCCTGCGGA CGCGG	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
5160	cg43984244	163	AGTGGGATGA GTGGCATTGCT GG[G/gap]ATATG GGGTAAAGTTG ATAAGGTC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5161	cg43984244	278	GCTCTAAAGCAG TCAGTGTACATT TT[gap]AGAGTG AAGAGGGGCATT GCAGGGT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5162	cg43984244	292	AGTGTACATTT AGAGTGAAGAG GG[G/gap]CATTG CAGGGTGCTAGT CCTCTTAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5163	cg43984244	302	TTAGAGTGAAGA GGGGCATTGCA GG[G/gap]TGCTA GTCCTCTTAAGC TCTGACCG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5164	cg43984244	69	ACTGAGGCACCA TATAAAGGGTTC C[G/C]GGAGTCT CTAAAGAGCTGG AGCTAC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5165	cg43993152	262	AACTCCTAACCT CAAGTGATCCGT C[C/T]GCCCTGG CCTCCCAAAGTG CTGGGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	

5166	cg43993152	270	ACCTCAAGTGAT CCGTCCGCCTTG G[C/gap]CTCCCA AAGTGCTGGAT TACAGGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	
5167	cg43018426	83	TGTAAAAACCAA TCACCTGCACAC A[C/gap]AAATTAT GTGAAATTAGTT TATATA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01344 INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) - Homo sapiens (Human), 180 aa.	4.3E-94	11 (1p15.5)
5168	cg43951338	304	ATCTCATTTTCTA ATCATGTGCTTT G[gap]AGACATTT AATACTATTTCAA TTAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5169	cg43951338	323	TGCTTTGAGACA TTTAATACTATTT [C/T]AATTATGCA GAGGAAATAATA TAAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5170	cg43951338	455	GTTCCCTCTCTT CAAACAGCTGGA G[C/gap]TGTACA CAGATGGAAAAA CATTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5171	cg43951338	468	AAACAGCTGGAG CTGTACACAGAT G[G/gap]AAAAAC ATTTGGTCAGAA AGCAGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5172	cg43954317	182	TTTCCCTTCTGAT GATTTTAAACTC T[gap]TAAAGAAC AGGAAAGCATCT GGTAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55957 BH3 INTERACTING DOMAIN DEATH AGONIST (BID) - Homo sapiens (Human), 195 aa.	3.4E-93	

5173	cg42669492	91	TGAAAAACATTT CAAAACCCCTCTA A/C/TAAAGTATTT AATGAAAAATAAA TTTAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34106 CGI-111 PROTEIN - HOMO SAPIENS (HUMAN), 199 aa.	1.3E-92	5
5174	cg43968495	1534	CTGGCTCAGCCCC CCGCAGACCTG CC/C/TACCCCTT TCTGCCACCCCC TGACGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5175	cg43968495	1597	CTCCCCCAGGC CTGCTGGGCACA CC/T/C/TATGCCA TCTCCCTCTCCA ACTTCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5176	cg43968495	1636	TCTCCAACITCA TCGGCCCTCAAGC C/T/C/GTGCCCTT CCTGGCTCTACC ACCTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5177	cg43968495	1646	CATCGGCCCTCAA GCCTGTGCCCTT C/C/T/TGGCTCTA CCACCTGCTTCC CCAGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5178	cg43968495	1652	CCTCAAGCCTGT GCCCTTCCTGGC T/C/T/TACCCACT GCTTCCCCCAGG GCCACC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5179	cg43968495	1675	CTCTACCACCTG CTTCCCCAGGGC C/A/G/CCGCCGG GCTTGGCGGCC TACACTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3

5180	cg43968495	1732	TGGCAGCGGCC AATGGGAGCAAG AA[A]G[GCTGAAC GGCAGAAATTCT CCCCCT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5181	cg43968495	1767	CAGAAATCTCC CCCTACTGAGGC C[G]A[GCTGAGG TACAGGCAGGG GCAGGCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5182	cg43968495	2254	TGTCAGGGGCG ACCCCAAAGAGG GG[G]G[CACTG CCAGGTAGCTG GGGGAGTGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5183	cg43968495	2286	CAGGTAGCTGG GGGAGTGGCAT GGG[G]G[CAAG GGCCCAGTTCTC AGCAGCAGA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5184	cg43973490	1222	TCCAATAGGAGT ATACTCTTTAATA [G]C[AACTGTATT TGAATAAGAATT CCAT	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa.	4.9E-92	
5185	cg43973490	2100	ATCTTCAGTGAT TCCTTGGCCTTC G[G]G[CTGCAG CTCCGAGGCGG TTTCCTCG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa.	4.9E-92	
5186	cg43979776	770	CCCGGTGCTGC CTGCTCTCATCC AG[T]C[TTCTTGG AAGAAATTTTATT CTGTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	

5187	cg43979776	791	CCAGTTTCTTGG AAGAAATTTTATT [C/T]GTTTCTCG TTTTCGGCACCA TGGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5188	cg43979776	797	TC TTGGAAGAA TTTATTCTGTTT [C/A]TCGTTTTCG GCACCATGGAAG AAAT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5189	cg43979776	802	GAAGAAATTTTA TTCTGTTTCTCG TT[C/T]TCGGCAC CATGGAAGAAAT GCAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5190	cg43979776	835	CCATGGAAGAA TGCAGAACAAAG C[C/T]GTGGTTT CTTTGTGTTTAC TCAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5191	cg43979776	856	AAGCCGTGGTTT TC TTTGTGTTTA [C/T]TCATGGAGC GCAATTGAAATT TTCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5192	cg43979776	858	GCCGTGGTTTTC TTTGTGTTTACT [C/T]ATGGAGCG CAATTGAAATTT CAGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5193	cg43979776	865	TTTCTTTGTGTT TTACTCATGGAG C/T]GCAATTGAA ATTTTCAGGTAC CCTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	

5194	cg43979776	887	GAGCGCAATTGAC AATTTTCAGGTA C/C/TCTTCTAC ATGCTGACGTGC ATTGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5195	cg43980242	1255	TTTTCCCTTTTTT TTTTTTTTTTTTTT gap]GTTGGCTTT GCGTTAGGATGC TC TG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
5196	cg43980242	411	GCAACTCCCAACG CAGGCCGCAAA GG[C/gap]GCTCT CGCGGCCGAGA GGCTTCGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
5197	cg43955549	222	TGAAACATACAA ATACAGAAAAAT A/C/A/CCCATTTA ACAAATACTAGT GTAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment).	1.7E-91	16
5198	cg43987971	40	TTTTTTTTTTTTT TTTTTTGGATGT G/A/TATTTTTT AATAGAAACCAC ATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa.	7.2E-91	1
5199	cg25236776	735	GCATACGGGGA CCACCTGTGTGC AC[C/gap]AGGAT GCCTGACACCAT GCTGCCCG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.2E-91	
5200	cg42527756	322	CAAGTACTGGAG CAGCTAGCAAGC T/C/T/ACTCCCCA CTCTCCTCACTT ATCTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q95221 PIUS - ORYCTOLAGUS CUNICULUS (RABBIT), 425 aa.	2.4E-90	3



5201	cg43937263	240	CCCCTTGGTTGT CGATGGTGTGGA A[C/gap]ATTGGG GTGAGGGGCAA AATGCCTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa.	2.4E-90	
5202	cg43937263	263	AACATTGGGGTG AGGGGCAAAATG C[C/gap]TAAGCA GAGCTGGAGGG AGGCAAAAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa.	2.4E-90	
5203	cg44015091	194	TATGAATTTTCTC ATGGAGATAGCA T[C]TTACATCAC AGAGCTGTTGTG AAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5204	cg44015091	210	GAGATAGCATTT ACATCACAGAGC TTG/AJTTGTGAAA ATAAAATAAGAA TGAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5205	cg44015091	231	AGCTGTTGTGAA AATAAAATAAGA AT/CJGTACAGCA CACCTGGAATAT AAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5206	cg44015091	256	GTACAGCACACC TGGAATATAAAA A[gap/A]CATCCC AATAACTTACTT GGAGCCC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5207	cg43963913	274	TTTTTATTATT TTTTTTTTTTTTT GJTGGCACAGAC GCGGGCTTTATT AAC	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11

5208	cg43963913	378	CGCAACGGTTAA ACCTGGCTCGC GA[C/T]TTAGCGC AGCGCCTGGG GGAAGC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
5209	cg43963913	511	CCGTGGCTTCAG ACGCACCGGAA GG[G/gap]AATCT GGGTCAGCCCT CCCTCCAAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
5210	cg43983527	1599	GCGTGCCTTTT GTGGACACAGG AG[C/gap]TCCTC CAGGAGCAGGC TGGGATCCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
5211	cg43003890	733	AGGAAAGCGATG GGGCTGCGCT GC[A/C]CACGTG GAGAGGGAGGG AGAGGGGA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14613 HYPOTHETICAL 22.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 210 aa.	1.3E-89	11
5212	cg43990642	1182	CCTGCCCCATCCT CCCATGAGAGAC TTC[G/T]TTGTTAGT CAACACATCTGT AAATA	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
5213	cg43990642	2175	TGTATTCTTGGT TCATTATAACAAA TC/TGTGTCGCTT AAATCCAAAAA AAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
5214	cg43916722	301	CCTGTGAGCATA TAAACACACAAA T[G/A]TATGTCG AAGTTGAAGATT AAGAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC78841 MYOTUBULARIN RELATED PROTEIN 6 - HOMO SAPIENS (HUMAN), 465 aa (fragment).	2.8E-89	13

5215	cg43059113	186	GATGCAGCTCAGG GGTACAAGGCA GT[G/T]TACAGG GTAGAGTGCAGC CCAAGCC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
5216	cg43922090	577	AAAAAAGGACCC AACTCTTACTTTA [G/A]GAGTATTAG GCCTGGACTTCC CCTG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5217	cg43922090	629	CCCATGCAATAA AGCAAGTTTTAT A[T/gap]ACACTC CCCATATTTTTT CTAACA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5218	cg43922090	923	TTGCTGTCTGTC CTCCAGAACCCG T[G/gap]CCAAGG CCTCCGAGTGCC CAGTTAC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5219	cg43922090	988	AGTTACTGAGGC AGCTGGGGAAAA A[C/T]GTTGAGTA AACATGATTCTA CAATT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5220	cg43960450	1307	GGGATTACTA TTGGTGGGCG TG[C/gap]CAGAC CCTCCCTTGCTT CAGCCAGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5221	cg43960450	1308	GGGATTACTAT TGGTGGGCGT GC[C/gap]AGACC CTCCCTTGCTTC AGCCAGAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8

5222	cg43960450	307	TTGGTGTGTTA GTAGGCAGGATT G[C/gap]CTTACA CTGGGGAAGAAA GACCAGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5223	cg43960450	308	TGGTGTGTTAG TAGGCAGGATTG C[C/gap]TTACAC TGGGGAAGAAA GACCAGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5224	cg43955651	110	GACAACACTCTT GAGCCTGCAGA GG[gap]CTCAG GCCACACCCACT TCTGCCGC	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5225	cg43955651	137	CACGGCCACAC CCACTTCTGCCG CA[G/gap]GGACT GTCTGTTGAGGA GCCGAACC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5226	cg43955651	139	CGGCCACACCC ACTTCTGCCGCA GG[G/gap]ACTGT CTGTTGAGGAGC CGAACCGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5227	cg43931874	307	CTTGGAGGAGG GCTGCCAAGTGT G[G/gap]CCAGGG GACCCGGCCTC AGGTCTGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	

5228	cg42556108	180	TGGGCTAGAGG GAGGCAGACAT GGG[G/gap]ACCA TGAAGACCCAAA GGGATGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49913 ANTIBACTERIAL PROTEIN FALL-39 PRECURSOR (FALL- 39 PEPTIDE ANTIBIOTIC) (ANTIMICROBIAL PROTEIN CAP-18) (LL-37) - Homo sapiens (Human), 170 aa.	2.9E-87	3
5229	cg43992520	165	TAAGCCTGCAGA GCTGTTTTTTTT [T/gap]CTACACA CGACAAATACTT TGATAT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5230	cg43992520	428	GGGAAGGGGC CAAGAAAAAAG AA[T/C]GGCCACT CTCCTTCTGTC CTTCCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5231	cg43992520	530	AGAAATCAATTG CACATCTCTAGT T[C/gap]GCAAGC GTCAAAGTCACA ACAAGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5232	cg43993006	58	CGGCCGGTCCA CTTTTTTTTTTT T[A/T]TAAGGTGT GAGCTTTTATTG CTTAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa.	7.7E-87	22
5233	cg43970868	855	TCCTGTCCCAGC CCTGCCTCCAGG G[C/gap]TCCTGG GCTGCCAGGGA CCTTCAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.8E-87	12

5234	cg43975606	1106	GAGAAATAGAAA GTCTTCAGTGAT G[G/gap]CCTACG CCAAAGCACAGG ATGGGGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa.	9.8E-87	X
5235	cg43975606	1132	CCTACGCCAAAG CACAGGATGGG GC[G/gap]GGCAG GAAGCCCTCTCC CAAGATCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa.	9.8E-87	X
5236	cg43068353	118	TGCTAGTGGTCC CTGCAGGCGCC GC[C/gap]GCGAC CGCCTCAGGGG GCCGTTGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
5237	cg43918822	1227	TAGGGATCACGC ATACCCCGAGACA G[G/gap]GCAGGC CCATCCTCAGGA GCTGCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5238	cg43918822	1266	CAGGAGCTGCA GTCACACTCAGC CC[G/gap]GCCTG AGGCAAGGGAT GCAGGGCCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5239	cg43918822	220	ACATTCCTTATTC TATTGCTTCAAA G/CJACAGTTTGT GAGAATGGAAGA TAAC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5240	cg43918822	500	AGAGTCTCCAC ATCTGCGAATGG G[G/gap]CCAATG GCACTCACTGTC TCTTCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15

5241	cg43918822	508	CCACATCTGCGA ATGGGGCCCAATG G[C/gap]ACTCAC TGCTCTTCAGG CCCCCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5242	cg44018226	342	GGCCAGTAGCT GCTGTGACCGA GTC[A/gap]CCAA GATGACCCACAGC AGGACCCTT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5243	cg44018226	426	GTCACGTCGTGA AGGCAGTGTGTG C[C/gap]TCTCGG CCGGCACAGGA GGGGCCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5244	cg44018226	638	CTTCCCTTCAG ATGTTATCTTTG G[G/gap]CCACCC GGCACTATTTT GGAATAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5245	cg43250258	617	TGCATTTCACAG ATAAGCAGGATT CTT/gap]ACATCC GGCCCCCAGTG CGTCTCGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa.	2.6E-86	2
5246	cg43312336	2475	AGAGTTCAGTGT TCGCAGTCGCAT ATT/ATACAACCA TGTTTCACACAG CCCTG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43532 RIG-LIKE 7-1 - HOMO SAPIENS (HUMAN), 171 aa.	7E-86	11
5247	cg43921099	211	TAAAGCTGGGTG TTGTCAGGCAAA G[C/gap]CCTTCC CTGCTGCCAGG GGTGGGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	

5248	cg43921099	213	AAGCTGGGTGTT GTCAGGCAAAGC C[C/gap]TTCCT GCTGCCAGGGG TGGGAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5249	cg43921099	293	CCCTCACACCCAC GGGAGGCAGCC CA[G/A]AGGCCA CCGGCACAGGG TGGTGGCC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5250	cg43921099	317	AGAGGCCACCG GCACAGGGTGG TGG[C/gap]CCCC AGATCATACAGC AGTGGGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5251	cg43921099	518	GTCAGTAGCACA TGGGCACCTGCT G[G/gap]CTTCTA GCCACTGCAGG CGGGCTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5252	cg43921099	612	CTAAAGTGCCC TGGAGGAGTGA GC[G/A]GCTGAC TGAAGCCCTCTG GGCACAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5253	cg43966448	1167	TACGCCTTTCAT CCCTCCTTCTAG G[G/gap]CCTATG GCAGTTCTCCCA GGATGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5254	cg43966448	1205	CTCCAGGATGT GTGGCGAGAGC CT[G/gap]GGCCA GCCCACAGCGTT CCTAGTCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22



5255	cg43966448	1207	CCCAGGATGTGTG GGCGAGAGCCT GG[G/gap]CCAGC CCACAGCGTTCC TAGTCAGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5256	cg43966448	1335	CTTCCAGCTGC TGTTTTGTAAAA [G/A]AAAAAGAAA AAAGAAGCCCAA ACTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5257	cg43966448	1551	AGAAAATGATTG ATGGGCTGGG AA[C/gap]CCTGG AGAGCCTCGACT CCGGAAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5258	cg43966448	959	TCCTGGTTCCT TGCCCGCGTGG GA[C/G]CCCAATA GAACTCAGCCCT TCCATG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5259	cg43923303	170	AAGTGTGGCACC AAAAGGTGGTAG GG[A/G]CGGCTG GGAGGGAGGA CCAGGAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O43709 PUTATIVE METHYLTRANSFERASE (EC 2.1.1.-) - Homo sapiens (Human), 220 aa.	2.3E-85	
5260	cg43948718	276	GATCAGTTTTGT ACAAGAGTTTTT TT[A/gap]AAAAAA TCAAATCACAAAC AAAGCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5261	cg43948718	378	CCAGTCTGCCT CTTCACAAACAC TTG[A/JATTCGGCT CTCCTAGGCTTC CGCCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17

5262	cg43948718	466	AAGTTAAGAGTG AGGCTGCTTCAG A[G/gap]CCCCCTG GCCCATGTGTCC ATCCAGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5263	cg43948718	494	CCTGGCCCCATGT GTCCATCCAGAC T[C/gap]CCAAGT GGAGTGTAGGG CTCCAGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5264	cg43948718	496	TGGCCCATGTGT CCATCCAGACTC C[C/gap]AAGTGG AGTGTAGGGCTC CCAGGGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5265	cg43934734	352	ACCACCCAAAGT CCTTTCAGGACC C[C/gap]AGGCCT GGCGGCTGTAG GAGAGAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5266	cg43934734	470	CTCCAGACAGGC CGGTGAGGCTA CT[C/T]GACACCC TCACAAAGGGGA AACCCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5267	cg43934734	547	CCCGATGCGGG AGGTTTTGGGCT AG[C/gap]CCTCC CCAGATCCCCG GCCTGAGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5268	cg44032523	19	TTTTTTTTTCAAT AAAAAA[gap]/A/C CATTATAGTCAT TTCATGTTGGT	gap	A				SILENT- NONCODI NG 955	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	9.1E-84	

5269	cg44032523	22	TTTTTTTTCATT AAAAAACCCAGJT TTATAGTCATTTC ATGTTGGTTGG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	9.1E-84	
5270	cg43945523	1372	AGATTAGCATTT TTCAACTGCTCA GTCCTCTCTCT CAATCTTGGAGA CATTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63918 SERUM DEPRIVATION RESPONSE (SDR=SERUM DEPRIVATION RESPONSE) - MUS MUSCULUS (MOUSE), 418 aa.	3.1E-83	2
5271	cg43919539	267	TCCTTTAAGAAG CCATTGATGGAC Cgap/CJTCATTG ATGGAAAGTTCT GTAAGTG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5272	cg43919539	4091	CCTCTCGGCTTA CAAGCAGGTCCT GAGJGCTCAAAA GGATGCAACCTT GACCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5273	cg43919539	609	AATAAATTTTCT TTTGTGTGTGT C/TJGAAITTTTACA GAAAAAAATACT GAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5274	cg43919539	844	GTCCAGGCCTAG GGGATGCTCTTC TTC/GJGAGCCTG TGCTGGTCTAGG AAGCCT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5275	cg43919539	879	CTGGTCTAGGAA GCCTCTTCTTTA GJGgapJAATCAT TTTTTTGTCCCC CGTGAAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1

5276	cg43989507	110	ATGCCCCCAGGTG GAAGATGTTTG C[G/A]GCTGTTCA GCAGCCACGTCT CCTGC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36639 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) - Homo sapiens (Human), 156 aa.	3.9E-83	7 (7p22)
5277	cg43988406	1748	TGTTGCCAAAAT GGTGGCCTGGC TT[G/gap]TCTTCT GAACGTTTGGTT CAAATGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E47283 DNA FOR ORF1 AND ORF2 FROM CHROMOSOME X - HOMO SAPIENS (HUMAN), 157 aa.	5E-83	X (Xp11.4)
5278	cg43948335	1456	GAAGATTCAACA CTCTGGAAGCT T[G/T]CAAAGATT ACTGTTCAACCGA GACAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P38714 ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.19) (ARGININE- TRNA LIGASE) (ARGRS) - Saccharomyces cerevisiae (Baker's yeast), 643 aa.	6.5E-83	6
5279	cg43970119	234	AATAATTATCTTG CGTAAAGAGAAA [A/G]GTAGAGCA CAATATATATATA TCAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1E-82	12
5280	cg43120215	256	AGGCCACCAGG AACTGTTTTTAAA G[C/A]ATAGGC TGCACTAGGAGG AAGTTT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.3E-82	7
5281	cg43120215	50	TTAATATCTAAGA TAAAAA gap/[A]CCCAACCA CCAAACAACCC ATTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.3E-82	7

5282	cg43921918	274	TGAAAGAACAAA CCAGAAGAATTT TTTATTTTCAGT TAGATTTTGAAG CTTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5283	cg43921918	275	GAAAGAACAAAC CAGAAGAATTT TTTATTTTCAGT AGATTTTGAAG CTTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5284	cg43921918	276	AAAGAACAAACC AGAAAGAATTTT TTTATTTTCAGT ATTTTGAACCT TTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5285	cg43921918	282	CAAACCAAGA ATTTTTCAG TTTATTTTCAG GAACTTTTATT TAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5286	cg43921918	404	GTATGTATCTGA TCCACACAAATC CTCTCTAATTTA TTTCTGTGTAG TCCTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5287	cg43921918	718	CTGTCTTGTTAA CCTCTCTAATTTA GTAJAAATCTGT GTCGTAAACT GGAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5288	cg43283313	961	GCGTCCGCTCC CCGGTCAGGAG CGCA/GGCCGA CGAGTACAGTTG CTGCTGCT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43658 CANDIDATE TUMOR SUPPRESSOR P33ING1 - HOMO SAPIENS (HUMAN), 279 aa.	1.9E-81	4

5289	cg43933199	470	TTTGGGGGGGTT GTGCTGGGGG GA[gap/G]GGG GTTCAAATATTTA TTGTATTT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa.	1.9E-81	19
5290	cg43933199	475	GGGGTGTGC TGGGGGGGAGG GGG[gap/G]TTCA AATATTTATTGTA TTTTTTGT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa.	1.9E-81	19
5291	cg44030987	83	CGTAAGCAGAAT TAACCAGACAGT TTT/AJCAAACTC GAACTTTGTTTA ATTAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa.	1.9E-81	
5292	cg43298483	100	CTAGGCTGGG CTGCCCGGCTCA GC[C/gap]AGCGG GTCTAAACAGTG TGTCAGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12
5293	cg43298483	215	AGTCGGCCCCCTA GTCGTGGGGA TT[G/A]GGCCAG GGAAGGGCAGG GCGGGGCG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12
5294	cg43298483	340	GGGTCGAGAG GGCGTGGCGGG CGC[C/gap]GGCC CCGCGCCCCCA GCGCCCCAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12

5295	cg43076394	184	ATTATATAATAA ATTCTTATGACA C/TJTGATTCCAA ATTGTATGTACG AAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5296	cg43076394	227	GTACGAAATTGGC TTGACATAATAA A/C/TJATAAACAT AAGGGCAATTTA AACAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5297	cg43076394	261	AAGGGCAATTTA AACATTGGCAGT A/G/AJTTTATGTA AGTCAATTCAAG GTCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5298	cg43076394	354	TCTTTAGGAAGC AGCCCTGTAACA A/T/CJGTACATTT GTAGATCAGGG GCTAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5299	cg43076394	48	AAAGTAGATTTT ATTACAGAGCAA A/TJTTTTCTATC AATCAATGCTTT AA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5300	cg43320682	299	CTGTCAAGCAGA TCTTGAGGGTTA T/G/AJGTTAAGCC TGATAACAGCCT CTTTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.6E-81	
5301	cg43321624	432	CAAGGGAGGGG ACAGGCACATGG AG(gap/CJTACCC GAAGTAGGGCA GGGTGTAGT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment).	1.1E-80	9

5302	cg42651270	281	CCGGTGAGGCC AGGGGCAGCAG TGC[G/A]GCTCA GCAGGTGCGAG GCAGGCTTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5303	cg42651270	88	TATTGAGCAGCT ACTGGGCAGTGA C[G/T]CTGCCGA GGCGGGAATCC CACACA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5304	cg42651270	92	GAGCAGCTACTG GGCAGTGACGC TG[C/gap]CGAGG CGGGAATCCCAC CACAGTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5305	cg43969140	222	ATTCCAAATTGCA GGGCCCCAGCA CA[G/C]GGCTGG GCAGGTGAGATA GGGAGGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5306	cg43969140	274	TGGAGGAAGTAA TCTGGCCCCAGG GC[C/gap]TCAGA GCTGTGAGATGA TATTGGGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5307	cg43969140	789	GGCTGCAGCGG CTCTGCTGAAC TG[C/gap]GGACC CCGCCAGACGC CCACTCTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	



5308	cg43270152	81	TCAATTTGGCTC TTCTTGGCTAAA A[A]gapJTCTCTG GAGGTGGTGG TGATGAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P39877 CALCIUM-DEPENDENT PHOSPHOLIPASE A2 PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) (PLA2-10) - Homo sapiens (Human), 138 aa.	4.6E-80	1
5309	cg43336199	139	TGCCCCCTTCCT AGGGTGCGGT GG[C]gap]CTCCA GCCAGGGGGC TTCAGGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
5310	cg43336199	140	GCCCCCTTCCTA GGGTGCGGTG GC[C]gap]TCCAG CCAGGGGGCT TCCAGGTTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
5311	cg43917480	788	TCCTTTAAAAG GAACAAACTTT A[G]T]TATTTAAT TAGTTGATTTATT TAAT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15849 THYROID RECEPTOR INTERACTING PROTEIN 3 (TRIP3) - Homo sapiens (Human), 152 aa (fragment).	1.6E-79	17
5312	cg42708544	123	CACACACACACA CACACACACACA C[A]gap]CGGATT CCCCATCAAGGG GACATTT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5313	cg42708544	124	CACACACACACA CACACACACACA C[gap/A]GGATT CCCATCAAGGG GACATTTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	

5314	cg42708544	341	GAAGACTGCAGC AAAGACATCCAA A[G/gap]CCAACG GCAAGGGAAGC GTCAGCGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5315	cg42708544	710	GCTACTCAGGAG GCTGAGGCGGG AG[A/G]ATCGCTT GAACCCGGGAG GGGAGG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5316	cg44024149	880	ATCCCTCACCCA TCCTAGAGGCCA G[G/gap]CAGGAG CCCTCTATACC CACCCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
5317	cg44024149	986	GTGCTTAACCAA AGAAGCTGTACT C[C/T]GGGGGT CTCTTCTGAATA AAGCAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
5318	cg43963131	186	CTGGGATGGATG AGTAAGAGGAG GA[A/C]GGTACA CTAGAGGCTTTG GTAAAC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5319	cg43963131	228	GGTAAACATCT TCTCTCCAGAG G[gap/G]TGAAGA TAAATAAACCTTA CAGAGA	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6

5320	cg43963131	318	TGGTTAGGGCA TCCAGGGGTGC C[C/gap]TTCCAA TGTGAAAGACAA ACTGTTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5321	cg43963131	331	CCAGGGGTGC CCTTCCAATGTG AA[A/gap]GACAA ACTGTTGCATCT TGCATCCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5322	cg43963131	369	CATCTTGCATCC TCATGCAAGGAA G[G/gap]AAGCAC ACTGCCTGGTGA GCCTGTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5323	cg43287619	186	CAATTAGAAAG AAACACACTTTA A[G/A]AAATCAAA ATTCTCAATTCA GGCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5324	cg43287619	517	TGGAGGCCGA GGTGGGTGGAT CAC[A/G]AGGTC AGGAGATCGAGA CCATCCTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5325	cg43287619	595	TAAAAAATACAA AAAATTAGCCGG G[C/T]GTGGTGG CGGGCGCCTGT AATCCCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5326	cg43287619	611	TTAGCCGGCGGT GGTGGCGGGCG CC[C/T]GTAATCC CAGCTACTCGGG AGGCTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12

5327	cg43287619	615	CCGGGCGTGGT GGCGGGCGCCT GTA[A/G]TCCCAG CTACTCGGGAG GCTGAGGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5328	cg43918538	1513	GGCCCCCAGG TGGAGTGCCTGA CA[T/C]JAGGGCT CGCTCCAGAGG CGTCTGAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5329	cg43918538	592	TTATTTTACTAT TAAAAA A/gap]TCAAAGGG ACACACTGGGAA TTGAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5330	cg43918538	592	TATTTTACTATT AAAAA gap/A]TCAAAGGG ACACACTGGGAA TTGAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5331	cg43918538	592	TATTTTACTATT AAAAA gap/A]TCAAAGGG ACACACTGGGAA TTGAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5332	cg43250517	206	TTTCAGATGATG GGGTCTGAGATG TTC/G]TCTCAGG CTGCATCAGCTG TCTTC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	1.4E-78	
5333	cg43267341	968	TTAGTCTTTTTT TTTTTTTTTTTTT[g ap/]TAAATCAATC TGAATCAGAAA GCGG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	

5334	cg43267341	1035	GTCTTGTCCTG TCCCCACTCATC C[C/T]TGGTCTGG TCCCCTGTTGCC TATAG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5335	cg43267341	1056	ATCCCTGGTCTG GTCCCCTGTTGC C[T/C]ATAGCCCT TTACCCTGAGCA CCACC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5336	cg43267341	1083	TAGCCCTTTACC CTGAGCACACAG C[C/gap]AACAGA CTGGGACACAG CCCCCTCG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5337	cg43267341	1092	ACCCTGAGCAC ACCCCAACAGAC T[G/gap]GGGACC AGCCCCCTCGC CTGCCTGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5338	cg43267341	1154	AACCCCTTTAGA TGGGAGGGAA GA[G/A]GAGGAG AGGGAGGGGA CCTGCCCC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5339	cg43267341	1167	GGGAGGGGAAG AGGAGGAGAGG GGA[G/gap]GGGA CCTGCCCCCTCC TCAGGCATC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	

5340	cg43267341	1170	GAGGGAAGAGG AGGAGAGGGA GGG[G]gap]ACCT GCCCCCTCCTCA GGCATCTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5341	cg43267341	1198	CTGCCCCCTCCT CAGGCATCTGG GA[G]gap]GGCCC TGCCCCCATGG GCTTTAGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5342	cg43267341	1200	GCCCCCTCCTCA GGCATCTGGA GG[G]gap]CCCTG CCCCCATGGCT TTACCCCTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5343	cg42535274	74	CCTGCTGCCACC ACCGCAGCCTC GG[G]gap]CTCCC AGGCGGACAC GGCCACCGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q43791 SPOP - HOMO SAPIENS (HUMAN), 374 aa.	1.8E-78	
5344	cg43999987	1703	ACACAGCCTGTG GATCCTGGGC AT[C]T]TGGAGG GCGCACACATCA GCAGCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q09981 HYPOTHETICAL 107.4 KD. PROTEIN F30H5.1 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 961 aa.	4.8E-78	15
5345	cg43949675	116	ACAAATCACAGC TGATAGACAGCG A[gap]A]CGCTTC CCCATAGAGACC GTGCTCC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5346	cg43949675	156	ACCGTGCTCCAA CTCGGGCCTGG GG[gap]C]ACTGC TCGCTGCTCCCA GGAAGGGG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	

5347	cg43949675	238	AGAGTCCAGGGT C GGAGCGCGCCA CC[C/gap]TCAGC CAGAGCAGCCA CGACAGCCA	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5348	cg43949675	910	CCGTCCCTCAG G AAGAACGAACGT G[G/gap]CGCCGC CTCCTCTCGGGA GCTCTCT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5349	cg43259701	605	GGACGAGTCGG G ACCGAGGCTAG GAC[G/A]TGCC GGCGCTCTCCA GCCCTGCAG	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00496 IPL (IPL) - HOMO SAPIENS (HUMAN), 152 aa.	1.3E-77	11
5350	cg44003673	110	GGGAACACCCC ACACCCACACCC TG[gap]/CJCCCC CATACCCCTTCC TCCAGGAG	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.6E-77	
5351	cg44003673	216	TCTCCAGTGTCT C GCTGCCTCCTCC C[C/T]GCAAAGTC TCCACAAAGCAC AGGAC	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.6E-77	
5352	cg44923000	291	TTTGTTCTTTTA T TATATACACATA T/CJTATCTCAAA ACATAGTTATTT TA	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12
5353	cg44923000	294	GTTTCTTTTATAT A ATACACATATTT A/JTCTCAAAACA TAGTTATTTTAC TT	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12

5354	cg44923000	665	AGGCATGAGGCT G GATAAAGAACGA A[G/gap]TTTTACT TTTTTTCATTAA ATAAG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12
5355	cg43112852	1152	CCTGACAAGCAC T CAGATTCCATTG TTT/AJTCACGTTT TTAGAGATTTAAT TCCA	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa.	1.1E-76	
5356	cg43112852	1153	CTGACAAGCACCC T AGATTCCATTGT TTT/AJACAGTTTT TAGAGATTTAATT CCAT	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa.	1.1E-76	
5357	cg42520895	97	AAGAAGGGCTCA G GGCCTCCCCG CC[G/gap]GGCCG TGGACAGAGGG GCACAGTTT	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB51858 ATP-DEPENDENT METALLOPROTEASE YME1L - HOMO SAPIENS (HUMAN), 716 aa.	2.4E-76	
5358	cg43298234	1052	GCTCCTGCCCTAC G ATCCAGGCAGAA A[G/T]ATAGGCAG GGGCTCTTGAA GACGT	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5359	cg43298234	1110	TGTGACCTCCGA G GCCCTCCTGGTG G[G/A]AAGACAG CTGGAAAGGCTG GGAGGA	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5360	cg43298234	1147	AAAGGCTGGGA C GGAGAAGGGAG GGG[C/T]TGGGG GTTCCCAGGAGC CATGCGTG	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7



5361	cg43298234	1260	CTGGAGTGGG GTGTGTTAGAGC CC[C/gap]TCACC GGGACTTGCTGT GCGGATGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5362	cg43298234	1287	CACCGGACTTG CTGTGCGGATG GG[G/gap]CCTGG GCCTCCTTCTTA CAGGGGCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5363	cg43298234	584	CACCGACACGCT GCTGTGAGGT CC[G/C]GGTGAG ATGGAGTGGGTC ACACCTG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5364	cg43298234	644	AAGAAAGTTCCC TGGGGATGGGA GA[G/T]CGGGTG GGTGCTGCCAAT CTCCAGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5365	cg43298234	825	CAGTGGAGGAAA ATGTGATAAGC C[A/G]GAGCTTGT GTGCTGGGCAC AGAAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5366	cg43298234	897	CGCAGGCTGGG CCGGAGCCTCT GCC[C/T]GCAGG TTTCTATGCTGTT TCTTAGC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5367	cg43957018	539	GGAGAGCATCA GGGCAGGCCTTT AG[G/gap]CTGTT GCTCTGGGCAG GGGGTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44697 MUM2 - HOMO SAPIENS (HUMAN), 145 aa.	2.1E-75	17

5368	cg43973471	128	TCCTGAGAACAA ACAAGTAGGCCT G[C/T]TCCTCTCA CCACGTGCTTGT TTATT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14834 DIM1P HOMOLOG - HOMO SAPIENS (HUMAN), 142 aa.	2.1E-75	
5369	cg43918219	387	GAGACAGTGTG GGCAATGGGG GG[C/gap]CCGCA GGCCTTCTTGT GGGCTGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5370	cg43918219	56	ATGGTCGATTT GTCTTTTCTTC T[ <del>gap</del> ]TTTTTCC CCATTTTTTCAA GGATG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5371	cg43918219	62	GATTTGTCTTT TTCTCTTTTTT [ <del>gap</del> ]CCCCATTT TTCAAGGATGGA AAGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5372	cg43311348	334	TTTTCTGAAAA AGACAGGCCCG GG[C/gap]CCACC CAGGTCCACTT CCACTCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22
5373	cg43311348	336	TTCTGAAAAAG ACAGGCCCGG CC[C/gap]ACCCA GGTCCACTTCC ACTCAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22
5374	cg43311348	66	TTTTTTTTTTT TTTTTTTTTTT[A /T]ACCTCTTCAG GATTATTGGGT CAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22

5375	cg44012742	1535	GGGTGACCACA CTGTACTTGGGG CTG[gap]GGCCC TCTGCCCTGTG TCCCATC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
5376	cg44012742	1537	GTGACCACACTG TACTTGGGCTG G[G/gap]CCCTCT GCCCTGTGTCC CCATCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
5377	cg43272466	714	CCAACCCATGAG CACTCAATTCCA C[AG]CAGGGGC AATACCTCAAGC AGAGAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5378	cg43272466	752	CTCAAGCAGAGA GAGGCTTCAG GC[C/gap]ACCCC ACTTCTGGCTCT TTCCAGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5379	cg43272466	766	GGGCTTCAGGC CACCCCACTTCT GG[C/TT]CTTTCC AGTCCTAGCAGG TAAAAG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5380	cg43984390	37	TTATGTTTACCA GTTTATTACAAA C[G/A]TTATTAGA AAAGGATACAAA TAAAGT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa.	1.9E-74	20
5381	cg43984390	811	GGCCAAGGACG GAATGACAGAAG AG[TT/GT]GATTAG TAACACACATATG GCTGTT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa.	1.9E-74	20

5382	cg42670378	154	TTATTTTAAATGA GAAAAAAAAAAAA A[gap]CCCTCACA ACGTGAGATTCC TTTAC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31392 GLYPICAN-6 - HOMO SAPIENS (HUMAN), 555 aa.	1.9E-74	
5383	cg43969639	965	CCACTCTGCAGT AAGGTGTTTCAA A[AT]CAGAAAAT GCACAAATGAAA AGTTA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5384	cg43969639	994	AAAATGCACAAA TGAAAAGTTAAC TTC/TJCCTACAGC ATGGTGTGGCAG GGGAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5385	cg43969639	995	AAATGCACAAAT GAAAAGTTAACT CIC/TJCTACAGCA TGGTGTGGCAG GGGAAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5386	cg43969639	996	AATGCACAAATG AAAAGTTAACTC CIC/TJACAGCAT GGTGTGGCAGG GGAAAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5387	cg43969639	1238	GCCTAATAGGTA TACTCTGGAAGC CIG/AJTAACAGGA AGCTACAATCAA ATCAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3

5388	cg42332174	1196	GAAAAGCTTATT CATGGCGGTGC AG[G]gap]CTGCA GCCTTCCCTCA GACCAGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5389	cg42332174	235	AAATTCTTCATG TCTTCTAACGTG gap/AJAAAAAAA AAATCCCATCC AATTA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5390	cg42332174	247	TGCTTCTAAGC TGAAAAA A[A]gap]TCCCAT CCAATTAACAA CTTTCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5391	cg42332174	247	GTCTTCTAAGC GAAAAA A[gap/A]TCCCAT CCAATTAACAA CTTTCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5392	cg42332174	37	CAGGATTATTA TAATGTTTCTT T/C]TTTTTTAG CTGAAATGTATT TTTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5393	cg42332174	39	GGATTATTATAA TGTTTCTTTT T/C]TTTTTAGCTG AAATGTAATTTA TT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5394	cg44007500	48	TTTTTTTTTTTT TTTTTTTTTTTTT AJATTGTATAAAA TTTAAATTTTATG A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45717 HYPOTHETICAL 17.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 153 aa (fragment).	1.4E-73	

5395	cg43981873	942	GGTTTGTGAA CGGCCGTCCA AA[G/A]CTGGCT GGATTCCTAGAA GAGICTG	G	A		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5396	cg43981873	1135	GCCTGCAGGGTT TCCTTGGGCGC GG[C/gap]CCCAA AATTGCCCTTCAA AACAAACC	C	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5397	cg43981873	1161	CCCAAAATTGCC TTCAAAAACAAAC C[C/gap]GGGACG GTTGAAAGCCTT CGAACCG	C	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5398	cg43981873	1201	CTTCGAACCGTG CAGGGGATGCC TT[gap/G]GGCC TGGCCCTTCGCT TCCTCTCT	gap	G		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5399	cg43981873	811	TGCTCAGAAAGG AAGAGGCAGGC GC[C/gap]AGGGG GAACCCCTTCG TGTTTTGT	C	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5400	cg43981873	824	AGAGGCAGGCG CCAGGGGGAAC CCC[C/gap]TTCG TGTTTTGTGACC CTCCCTTTT	C	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5401	cg44004729	287	TTTTCTTGCTTGA CACTTTATTCTC[ G/C]TGAGAGGG GAGGACAGCAG AGGGAG	G	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	

5402	cg44004729	379	CGGAGGAGCCG GCAGAGGTGCT GA[G/C]GTTCCC GGGATCTGAGG ACAGGAGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	
5403	cg43942549	2079	AGAAGAAAGCAA GCAAGGCCGCTT C[C/gap]TGCGGC TAAGTGGACAGG CGACTGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94218 CODED FOR BY C. ELEGANS CDNA CM10H5 - CAENORHABDITIS ELEGANS, 589 aa.	2.8E-73	4
5404	cg43933021	240	CTTTTTTTTTT CGAAGTCCCTC [T/gap]TTTTTTT CCTTCAGTGTGG TCCTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
5405	cg43947751	220	GGATCCTTTTGA GATCATGCTCCC A[C/gap]ATCTATT AAAAGATACATA AGCTTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91086 CODED FOR BY C. ELEGANS CDNA YK134H12.5 - CAENORHABDITIS ELEGANS, 470 aa.	8.6E-73	6
5406	cg43048518	226	GTGGATGTCATT GAGCCTTGGA GG[C/gap]CCCAG TCTGGCGGGAG AGAAATCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTI-L) - Homo sapiens (Human), 773 aa.	2.5E-72	19
5407	cg43048518	229	GATGTCATTGAG GCCTTGAGGC CC[C/gap]AGTCT GGCGGAGAGA AATCCACAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTI-L) - Homo sapiens (Human), 773 aa.	2.5E-72	19
5408	cg43932428	386	ACAGCAGGAATG GGCTGGGGAGG GT[C/gap]CCCCG CAAGCTGGACCC CTTGTTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	

5409	cg43932428	426	CCCCTTGTTCGG TTCGGCCCGTGA G[G/gap]AGAACG GAACTGGCGGC CAAGGGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	
5410	cg42372763	150	ACTGGGAAAGAT CCGAGGTCAGG AA[T/G]AGGCC GTCAATCAGAAG CGCTGAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75128 KIAA0633 PROTEIN - HOMO SAPIENS (HUMAN), 1316 aa (fragment).	3.3E-72	7
5411	cg43981956	854	GAGTGGCGGGA AATGGGGGCA TCA[C/G]CATGCC TGCCGTCGGTT CCTGCGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63625 CTD-BINDING SR-LIKE PROTEIN RA9 - RATTUS NORVEGICUS (RAT), 1473 aa.	1.6E-71	
5412	cg43292786	825	AAGAAAACACAA CTGTACTTTAAA A[T/C]ATGTACAA AGAAAAAATTT CTTTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82970 AP-4 CLATHRIN ADAPTOR-RELATED COMPLEX SIGMA4 SUBUNIT - HOMO SAPIENS (HUMAN), 144 aa.	1.8E-71	
5413	cg43951096	1405	TCTGGTTATCTA CCTATAAATTTCA [T/C]GGTATTTCT TTAAACACTGAA GTAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
5414	cg43951096	1423	AATTCATGGTA TTCTTTAAACAC [T/A]GAAGTACTA AAAGCACTGATG ATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
5415	cg43951096	456	CCCATGTGAAAA GTTTCCATGCAG TT[gap]ACAAAG GCAGCAGCACAT GCTGTTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17



5416	cg43934599	582	GGCCAGGCCAG AAGAGTAAGGC AA[C/T]TCAGGAT ACTCCATTATT GAATC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa.	3.7E-71	10
5417	cg43283970	1054	CGGCCCTGCCG TTTAACCCGGCC CT[A/C]AGAAGAG TGAACACAGAATC CAAATC	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82971 KIAA1019 PROTEIN - HOMO SAPIENS (HUMAN), 1867 aa (fragment).	8.1E-71	21 (21q22.1 )
5418	cg43271682	112	CGTTGCCCCCCC CCGCCCCCGCC CC[A/G]CATGCTC TGACTCCTTTGG GGTCTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5419	cg43271682	650	TCAGTCCTGGCC TGGGCAGGAGT CT[G/gap]GCGGA GCCTCTGAGGTG ACGAGACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5420	cg43271682	651	CAGTCCTGGCCT GGCAGGAGTC TG[G/gap]CGGAG CCTCTGAGGTGA CGAGACCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5421	cg43271682	90	AGCGCCCCCTC CCTTAGCCCTAC GT[T/C]GCCCCC CCCCGCCCCCG CCCCACAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5422	cg43271682	96	CCTCCCTTAGCC CTACGTTGCCCC C[gap/A]CCCCGC CCCCGCCCCAC ATGCTCTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1

5423	cg44032365	203	AACAAAAATTTAA AAAATCACCTAT T[gap]ATCTTACC ACACAACCACTG TTATG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15170 (PP21) - HOMO SAPIENS (HUMAN), 157 aa.	3.3E-70	
5424	cg43918399	1015	TGCTGTTCTACT ATTTAACTACTG [G/gap]CAAAAGCC ACTTGCAITTTTC ATTAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q43415 HYPOTHETICAL 15.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 136 aa (fragment).	4.2E-70	4
5425	cg43045396	102	TAGGATACAAG AGGCACCAAGG CC[T/A]GGGGG TGGGGGTGGG GACACTAC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5426	cg43045396	216	AGCTCAGAACTA TGACATAATTCCT C[A/gap]GGGGAG CCTGCATCCCT CCTGAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5427	cg43045396	222	GAACATGACAT ATTCCTCAGGG A[G/gap]CCTGCA TCCCTTCCTGAA AGTAGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5428	cg43045396	266	AGTAGGAGCAAG CCAGCTGCCTC A[C/T]TCTCGGAC ATAAATTCTGGT GCAGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5429	cg43045396	63	ATGACTTCGAAA CCGTGCAAATGC C[A/G]AACTATGG AGCACTAGGGAT ACAAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15

5430	cg43045396	64	TGACTTCGAAAC CGTGCAAATGCC A[A/G]ACTATGGA GCACTAGGGATA CAAGA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5431	cg43045396	65	GACTTCGAAACC GTGCAAATGCCA A[A/G]CTATGGAG CACTAGGGATAC AAGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5432	cg43045396	71	GAAACCGTGCA ATGCCAAACTAT G[G/C]AGCACTA GGGATACAAGAG GCACCA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5433	cg43917991	400	CCTGAGAGGGT GACAGTCACAGC TA[C/T]AAAGAGA GGGCCGAGCTC CTGGTGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	6.9E-70	11
5434	cg43967210	379	ACCTCAAGAGAG AGCTAAATCAAT TTC/TJAGGTTTTG GAAAAATTTTATT GCAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O44780 CODED FOR BY C. ELEGANS CDNA YK355D7.5 (CODED FOR BY C. ELEGANS CDNA YK373A5.5) - CAENORHABDITIS ELEGANS, 885 aa.	8.1E-70	3
5435	cg44922306	482	ATAAGATAAAT GAACACAGTAAT G[A/gap]AAAAAA AAAGAAAGAAAC AGTATGG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17

5436	cg44922306	491	ATTGAACACAGT AATGAAAAAAAA A[A]gap]GAAAGA AACAGTATGGAG ATTGCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17
5437	cg44922306	491	TTGAACACAGTA ATGAAAAAAAA A[gap/A]GAAAGA AACAGTATGGAG ATTGCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17
5438	cg42500321	110	CCAGGGCCTGA CTTGGCAGTGGC CC[C]gap]AGGCT GCATGGGCTCA GGTAGGCTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41588 TESTISIN - HOMO SAPIENS (HUMAN), 314 aa.	2E-69	16
5439	cg40985789	549	GGCGTTTCCAA GTCATTTTATCA [A]G]AATTTTG TTTGTTCCCTGA ATCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P04765 EUKARYOTIC INITIATION FACTOR 4A-I (EIF-4A-I) - Homo sapiens (Human), and Mus musculus (Mouse), 406 aa.	2.6E-69	17
5440	cg43292900	285	TTATTCAGAATC ATAAGGGTTTT TTA]T]AAAAAAT CTTACCATTATG AAAGT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75449 P60 KATANIN - HOMO SAPIENS (HUMAN), 491 aa.	3E-69	6
5441	cg43930848	1334	GGTGGGGGTAA TTGTCTCTTGGT GG[G]gap]CCCAG TTAGTGGGCCTT CCTGAGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.9E-69	7 (7q21)

5442	cg43323149	1471	TCGGTCTTTTA GTTTAAATTTATT [G/A]GTAAACTG ATGGCAGCAATC CATG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1E-68	1
5443	cg41400057	183	AATGGTAGTCAC TGTGAAAACTGC TTTCTCTAAAC ACAGGCTAGCC TGACT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa.	2.7E-68	9
5444	cg43955219	625	CATCTCTCCAC TGATGCGCGTG C[C/gap]TAGACC GATGGCAGCCAT CGAATAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
5445	cg43955219	681	GGGTGTTTCCA A CCCCCTGCAG CA[AC]CTAAGAT GGTGGGGAGA GGGGTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
5446	cg44004331	138	CAGACAGCAGG C ACTCCAAAGAGG GT[C/G]GGCCTC CTAGGCTGCCCC GGACTAG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5447	cg44004331	234	GAGGGACCCC C TGACCTGCCTCT GG[C/gap]CGCCG AACCCGGGGCC CTCCCCCTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5448	cg44004331	296	ATCTCAGAAAC G AAAGGCTGTCCC T[G/T]CTTTGTC AGCCCTAGACCA GGTCT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	

5449	cg44004331	35	TTTAGATTTTGT CTACATTTTATT C/TTTTCACTCAA CAGAAATAGAAGT TTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5450	cg43980385	286	ACTGCTCAGCCT GGTGGTGGCTG GA[G/C]CTCAGA AATTGGGAGTGA CACAGGA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
5451	cg43989533	35	TTTTTTTTTTTT TTTTTTTTTTTTT A/GAATTTTAAAA AGCCATTTATTT A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
5452	cg43989533	37	TTTTTTTTTTTT TTTTTTTTTTG[A /TTTTTAAAAAG CCATTTATTTAA A	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
5453	cg43951170	241	TCTAATTTCTGGG TTCTGCACCATC A[G/A]GAAGAGA ATATCCTACAGG ACAGTT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa.	1.9E-67	13
5454	cg43951170	260	CCATCAGGAAGA GAATATCCTACA G[G/T]ACAGTTCT CCTTGATACTG CATAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa.	1.9E-67	13
5455	cg44921579	625	GGCTTAGAAGAT GAACCCCTTGAG A[T/C]GGCCACTA AGGAGAATTGAA AAAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75477 KE04P - HOMO SAPIENS (HUMAN), 346 aa.	3.1E-67	

5456	cg44030323	422	AGCCTGGGTCA GAGGCCTGGTG GGC[C/gap]AGCC CAGTGGGACTAG GCAGGAAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27747 CGI-38 PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	3.9E-67	
5457	cg43999983	875	GATTCCACCTG TAATCATAACTT [G/T]TTAACATCA AACTCGACAGCT AACC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa.	1E-66	
5458	cg42506346	532	TCAGAGATGAAA AGTCACCTCAGT T[gap/T]JAAAAGC AAAAAGGAAGAT AGAAAAT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45744 HYPOTHETICAL 66.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 577 aa (fragment).	3.5E-66	2
5459	cg44928538	1092	CCGCCCCACTA TGGGCCTACCAT T[A/T]ATAGTGT TAAC TTGGAGGT TAAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa.	3.5E-66	7
5460	cg44928538	917	GGTAAAACATT TTAGAAATATTCT [A/T]GAGATGGG CAGGAGAGTCAA AGGGC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa.	3.5E-66	7
5461	cg44911411	1159	GGGTTTCTGCC ACTCCGGGTCT A[G/gap]GCCCTG CCCCAAATCCAG CCAGTCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5462	cg44911411	1160	GGGTTTCTGCCA CTCCGGGTCTA G[G/gap]CCCTGC CCCCAAATCCAGC CAGTCCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	

5463	cg44911411	1166	CTGCCACTTCGG GGTCTAGGCCCT G[C/gap]CCCAAA TCCAGCCAGTCC TGCCCCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5464	cg44911411	714	TTCTGGATCCCA CAGTGTATGGA G[C/gap]CCCTGA CTCCTCACGTGC CTGATCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5465	cg43984044	948	CCTTCCCTCCT GGATTCGGGTA G[C/G]AGAGCA GCGCCGCAGGA GGCGGT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.3E-66	19
5466	cg43984044	960	GGATTCGGGTA GCAGAGGCAGC GC[C/gap]GCAGG AGGCGGGTGCC CGTTTGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.3E-66	19
5467	cg43989609	192	AAAAAACCAAC AAAGATTTTTTT [C/T]TTGTATTG CAGGACAAAGTAC AACT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	
5468	cg43989609	195	AAACCAACAAA GATTTTTTCTT [G/T]TATTGCAG GACAAGTACAAC TGAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	
5469	cg43989609	329	CTTTGTATATT TACAGGCAAAA G/AJAATGATTCC TCAGCAGTCATT GTGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	



5470	cg42871015	100	CAATGAATTATT ACCTCAATATC[ A/gap]AGAGGCC CTGAGGTAGGGT GGCTCC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O08616 BETA-ALANINE- PYRUVATE AMINOTRANSFERASE PRECURSOR - RATTUS NORVEGICUS (RAT), 512 aa.	2.5E-65	5
5471	cg43919145	346	AAAAATGCACTA AAGCTCTGTAAA G/gap/AJAAAAAA TATAATAAATGTC TTATAC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.2E-65	1
5472	cg43919145	352	GCACTAAAGCTC TGTAAGAAAAA A/gap/AJTATAATA AATGCTTATAC AAATTT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.2E-65	1
5473	cg42703392	20	TTTTTTTTTTTT TTTTTT[G/T]TCA GAAGTAGGGTTT TGTTTATTAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q60778 NUCLEAR FACTOR OF KAPPA LIGHT CHAIN PROTEIN ENHANCER IN B-CELLS INHIBITOR, ALPHA (Kb-BETA) - MUS MUSCULUS (MOUSE), 359 aa.	4.2E-65	
5474	cg43946737	229	GGCGCGCGAGG AGGCTGGCTGG GGC[C/gap]ATCA CGGAGTGCCCAT CCTGCACTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42836 DJ22E13.1A.1 (C- TERMINAL PART OF NOVEL PROTEIN DJ22E13.1) (PARTIAL ISOFORM 1) - HOMO SAPIENS (HUMAN), 134 aa (fragment).	1.1E-64	22
5475	cg43923225	1058	AAAGTGACCCCTA TAGCGCAGGGA GC[G/A]GGGTAG TTCCTTGGCTTT ATGCAIT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5476	cg43923225	1150	GATGGTTGTTAT TGAGGATGGGG TG[G/gap]CCATT GGCTAGGGGCC GGCTCTTTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1

5477	cg43923225	258	ATTTTATTTAA TCCTTTAATTTT[A /TAAAAAAACCC CATTAAACAGTAC ATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5478	cg43923225	458	GGGGAGAGG CCAGAGAAAGGA GG[A]gapjGGCAG TCAGATCTTAGA CCTGTCGC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5479	cg43929282	128	TGATCATCACAT GAGCCCTCTTCT C/C/TATATACAC ATTGTTAGTGT GAAAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa.	2.9E-64	
5480	cg43929282	301	TAAAGGAAAATT TCCCATCCAGTC A/T/CJTGAGAAAT GCTAAAGGCATT TTATG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa.	2.9E-64	
5481	cg44924736	1579	TTTTTTTTTTC ACATTACCGAAAT G/gapjGCCAAGT AATGTGGTGTGA TTACTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa.	5.6E-64	3
5482	cg44924736	1580	TTTTTTTTTTC CATTACCGAAAGT G/gapjCCAAGTAA TGTGGTGTGATT ACTAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa.	5.6E-64	3
5483	cg42381630	643	GTTTCATTAAAATT CTCCCAATAAAGT C/gapjTTTACAGC CTTCTGCAAAAA AAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	

5484	cg42381630	662	ATAAAGCTTTAC AGCCTTCTGCAA A/A/GJAAAAAAAA AAAAAAAAAAAA AAAAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
5485	cg44001502	1002	GATTATTATTG TAATACCTCACAJ G/AJACGTTGTAC CATATCCATGCA CATT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
5486	cg44001502	1009	TTATTGTAATACCT TCACAGACGTTG [T/C]ACCATATCC ATGCACATTTAG TTGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
5487	cg42367764	486	ATTCACACACCTC TCTTCCCCAGCC G[ap/G]CAACGG GGGTGCCAGGA GCCCCAGG	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa.	9.7E-64	8
5488	cg42367764	622	AGGATGAAGCCA CCCCACAGAGG AT[G/gap]CAGCC CCCAGCTGCATG GAAGGTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa.	9.7E-64	8
5489	cg43132517	399	GGTTAATAAATT ACTAGGTCTATT T[T/C]GAATAACA AATTGAGTACTT TTATT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5490	cg43132517	419	TATTTGAATAAC AAATTGAGTACTI T[C]TTATTAGACC TAAGTGAACCTT TAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	

5491	cg43132517	424	TGAATAACAAAT TGAGTACTTTTAT [T/G]AGACCTAAG TGGAACCTTTATC TGAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5492	cg43132517	442	CTTTTATTAGAC CTAAGTGGAAC TTT/CATCTGAAT CTGAATTTTCCA AGGGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5493	cg43969715	284	CAGTTTCTTTCA CAAAACAGCATT CIG/AJAGGAGA AGGGAAAGTTCC CACATT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60888 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa.	3.3E-63	22
5494	cg43933863	284	ACGTATTAGGAA CAAAATTAAGAGT TTT/AJTTTTGGG TTTTAAACTGCA CTTTA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa.	1.1E-62	
5495	cg43933863	286	GTATTAGGAACA AATTAAGAGTTTT [T/A]TTTGGGTTT TAAACTGCACCT TATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa.	1.1E-62	
5496	cg43950549	1039	GGACGGGCTGA ACCAGCGCTACT TC[C/gap]GCAAG CGTGCCCTCTAC CTGGCCCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
5497	cg43988710	64	ATCTTGTGGGA CTCTTTTGCCTA A[G/C]CTGGTTCC CAAATCATGGAG GGAAA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	

5498	cg43308257	1097	CGACGTTTTCGGG CAGTGTTCCTTG T[Gap]CCCGTG GGCCGGGAGC GAGTAAAG	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5499	cg43308257	1135	GGAGCGAGTAA GTCTGGGCCAG GC[AT]AAAAA AAAAA AAAAA	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5500	cg43308257	439	TGAGCGAGATT CTACAGTGAGAT C[CT]TGGACAAG AAGTTCACAGTG ACTGT	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5501	cg44015973	1734	AAGAAGAGGCCT CCATTTTTTTTT T[Gap]CTTTTTTT ATTGGTGTAGTT ACGA	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	3 (3p24.2)
5502	cg44015973	2224	GTAAAGTAA ACTTTACCATGC C[Gap]TTTTTTT TTTTGTGGCC TAACAT	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	3 (3p24.2)
5503	cg44015973	2225	GTAAAGTAA ACTTTACCATGC C[AT]TTTTTTT TTTTGTGGCCT AACATT	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	3 (3p24.2)
5504	cg44015973	2236	AACTTTACCATG CCTTTTTTTTT T[Gap]GTGGCCT AACATTGAGGCC TTAA	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	3 (3p24.2)

5505	cg43981475	211	CTGGAAGAAG CTGTTGTCGT TTT[ <i>gap</i> ]GATTGT CCTCTGCCAGCA GATCTGC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	4.8E-62	
5506	cg43981475	415	TCCGCTCTTTTC TGGCCCTGGAG GC[C/ <i>gap</i> ]ATGAG GCTGAAGAAGAG CCCAGGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	4.8E-62	
5507	cg43950850	41	CAATGAGACTTT ATTGGCAGTGGG C[C/ <i>gap</i> ]JAGATT GGTAGTCTGCT AACTCTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (C1-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11
5508	cg43961684	192	CAAAATAAAAAG ATCCACGTTCT T[AT]TTCTCTAC ACAAAACGCGTT TTTAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19
5509	cg43961684	44	TTTTTTTTTTT TTTTTTTTTTT[G /T]TGTTCCAGA AGAGAAATTTAA TCT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19
5510	cg43961684	46	TTTTTTTTTTT TTTTTTTTTTT[G] G/T]TTCCAGAA GAGAAATTTAAT CTAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19
5511	cg43961684	466	CATTGTGGGCTC AGTGGGGGGCT CC[C/ <i>gap</i> ]AGGCC CCAGCAGGCCC CACAGAGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19

5512	cg43983897	339	CAAGATACCGAC TTTCTGGCCCTG G[C/gap]CCTAAT CCTAAACTCTCC TCCTTTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5513	cg43983897	341	AGATACCGACTT TCTGGCCCTGGC C[C/gap]TAATCC TAAACTCTCCTC CTTTGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5514	cg43983897	377	CTCTCCTCCTTT GCAAGCTGACAA A[G/T]CAAGGATT TGATATGTCTCGA GAGGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5515	cg44926530	1746	ACACTGACAAAT TCCTTAAGTTAAT G[G/gap]CTTTAG CCCAACATTTT AGTCAGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5516	cg44926530	213	AGGGCACAAAAG CCAGCAGCATAA A[gap/A]GAAACA TGAATAATGACT GAGAATT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5517	cg44926530	368	CAACATGCACA TAGTATTCCTAC A[A/T]GAATATTG CCTTAATATTGT CAATA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5518	cg42701870	133	TTGCTTTGAGAG TGATGCGATGTA TG[A/T]ATATATA TGATAAATGATT ATAAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q07325 GAMMA INTERFERON INDUCED MONOKINE PRECURSOR (MIG) - Homo sapiens (Human), 125 aa.	3.4E-61	4

5519	cg43918476	1426	TGAAATAACTGG GTTTAAAAAAA A[A/gap]GTTTAA ATGAAGCCCAAG TTTAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.3E-61	2
5520	cg43918476	174	TATTGTGACAGC AAATGCACATAG TTG[gap]CTGTAG GTAAGGCATGCT ACTAGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.3E-61	2
5521	cg43298020	572	CTTGAATAAAAC ACAAGCCTCCGT TTATJAAAAAAA AAAAAATAAAAA AAAGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
5522	cg43982373	27	GTCGACTTTTTT TTTTTTTTTTTT[G /TTGAGCAACAG AGATAGTCTTTA TTC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38195 MINDIN PRECURSOR - RATTUS NORVEGICUS (RAT), 330 aa.	8.8E-61	4
5523	cg43285334	364	AAGAAGGTTCTT CTAGGAGGCC CG[C/gap]CCCTC CAAATGGTCATT TCCTCTTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
5524	cg43285334	367	AAGGTTCTTCTA GGAGGCCCCCGC CC[C/gap]TCCAA ATGGTCATTTCT CTTTCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
5525	cg43285334	795	GTCAAAGCCCTG GGCGCAGCAT GC[C/gap]TACGG TTCCTAACCCCTG GGCTTTTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1



5526	cg43919806	592	AACTCAGGAGGCA AGAGGCTGCAGT G[A/G]GCTGAGA TTGCACCACTGC ACTCTA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O18216 Y53C12B.2 - CAENORHABDITIS ELEGANS, 277 aa.	2.3E-60	2
5527	cg43916931	1543	TTGCATTTTATT CAAATGTTATCT C/gapTTTTTTTC TTTGAGAAATAA ACTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa.	9.5E-60	1
5528	cg43916931	1827	TATATGTAATTG TGTTGTTAAAGAG C/GTGTACTACTGA TTTTCATATGACA ATG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa.	9.5E-60	1
5529	cg42886005	106	CAAAGAGAACAG GAATGGCTGACT C/T/C/GCATAAAT TGGCCGAAGATT ATCCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa.	1.3E-59 (11q13.3)	11
5530	cg42886005	174	TTCAGGTTACAG CACACAGACAAA C/G/A/TGCCCCAG GAGGCTCTCAG GACCGCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa.	1.3E-59 (11q13.3)	11
5531	cg43985327	68	TTTCCTTTGTCC AGTTCCTTTATT G/TGGGGCAGG GCACCAAGAAGA GGCCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
5532	cg43985327	80	CAGTTCCTTTATT GGGGGCAGGGC A/C/gapCAAGAA GAGGCCCTCCG CTCCCCAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1

5533	cg43958640	105	GGAGCCCCACG AATGTGAGGCCT GG[C/gap]CCCTT CCTCCAGGCCTC CAGGCCCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa.	2.7E-59	
5534	cg43958640	99	ATTCAGGGAGCC CCACGAATGTGA G[G/gap]CCTGGC CCCTTCCTCCAG GCCTCCA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa.	2.7E-59	
5535	cg43978473	190	GACGGGCCCC CCATGCTGTCGG GG[C/gap]CCAGG GCTGCTGTCCGC AAAGAGCG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11
5536	cg43939569	895	TCITTTGTACAG AACTTCATCCTC C[C/gap]GGGAAC CGGGCTGGACA GGGCTGGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
5537	cg43939569	357	AGAAAGGAGAAA GGAGAGTTACAA G[A/T]TGCCAACT CCACCATTACCC CTCCT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
5538	cg43253949	531	GTCGACTGTTGC TTGCTGGTCGCA G[A/gap]CTCCCT GACCCCTCCCTC ACCCCTC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12

5539	cg43253949	628	CCCAGCCCTAGT GTCAGGGCGGG GG[C/gap]CTGGA GCAGCCCGAGG CACTGCAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5540	cg43253949	710	CTCGCCAGTCCG GTCGCTGGCTTC G[C/gap]GCCGCC ATGGCAATGAGA CAGACGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5541	cg43253949	710	TCGCCAGTCCG GTCGCTGGCTTC GC[gap]C]GCCGC CATGGCAATGAG ACAGACGC	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5542	cg44011422	883	AGGCCACCCTG CCTCTACCCCAAC CA[G/gap]GGCCC CGGGCCTGTGA TGTCAAAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5543	cg44011422	885	GCCACCCTGCCT CTACCCCAACCAG G[G/gap]CCCCGG GGCCTGTTATGT CAAAC TG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)

5544	cg44011422	895	CTCTACCCAACC AGGCCCGGG GC[ <i>gap</i> ]TGTTA TGTCAAACTGTC TTGGCTGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5545	cg44011422	806	CAGTGGCCAAGA TCACAGTGGCCA C[ <i>gap</i> ]GCCACG GCCACAGTCATG GTGGCCA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5546	cg44011422	807	AGTGGCCAAGAT CACAGTGGCCAC G[ <i>gap</i> ]CCACGG CCACAGTCATGG TGGCCAC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5547	cg44011422	834	CACGGCCACAGT CATGGTGGCCAC G[ <i>gap</i> ]CCACAG CCACTAATCAGG AGGCCAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5548	cg44005977	604	AAAATCTGTGGT ATAACAATGTAC T[ <i>gap</i> ]ATGTTCTG TAGCTCTTTACT GAAGG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76071 WD40 PROTEIN CIAO 1 - HOMO SAPIENS (HUMAN), 339 aa.	4.4E-59	

5549	cg43063845	740	GTATTCCGGATT AGCAACCCAGGA A[A/C]CCATCACT TCTGAAGACTCT AAACT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O57683 146KDA NUCLEAR PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1307 aa.	5.4E-59	
5550	cg44914411	778	GTCCCCCAGGCT GGAGTGCAGTG GC[G/A]CGATCAT GCTCACTGCAGC CTCAAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5551	cg44914411	803	GCGATCATGCTC ACTGCAGCCTCA A[T/C]CTCCTGGG CTCAAGTGATCC TCCTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5552	cg44914411	891	CCACCGTGCTG GCCTCTATTCTT GT[C/A]ATTGAAT GAGATGCTATGA GGCCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5553	cg44914411	915	GTAATTGAATGA GATGCTATGAGG C[C/G]CTGAGCG ACCCACAGGAAA GTACTT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5554	cg43959535	322	TGACITTTGAAG ACGTGGCTGTGA A[C/A]TTTTCCCA GGAGGAATGGA GTCTCC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92967 ZINC FINGER PROTEIN ZFP6 - HOMO SAPIENS (HUMAN), 431 aa (fragment).	9.2E-59	19
5555	cg43924537	126	AGTGCTCGACTT TCTGGTGGCAG GG[C/gap]CCAGA GCTCACGGACAC CACTGACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	

5556	cg43924537	128	TGCTCGACTTTC TGGTGGCAGGG CC[C/gap]AGAGC TCACGGACACCA CTGACAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	
5557	cg43924537	55	TTTTTTTTTTTT TTTTTAGAAA T/A/AACTCTTGT ATTGTAGCACAT TTC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	
5558	cg43986278	2035	TCTAAATGAATTA CAGGTACAGATG [G/T]TATGCTAGG TGGAGTATGCTT GATA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q60395 PAC CLONE DJ0911H05 FROM 7Q21-Q22, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 133 aa (fragment).	1.9E-58	7
5559	cg44915744	710	ATACAGAGTTTT ATTTGAGTTTT [C/T]TTTTTGTGC ATTGTCCTCATG CCTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa.	1.9E-58	16
5560	cg42717343	615	AAATGCTGTGCC AGGCATCTCTAA G[C/gap]TCTGCC CTTACTCTGTGT GGGTTTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa.	1.9E-58	
5561	cg42346579	137	CTGCGATCACTC CAGCCGGTGTG GT[C/T]ACAGCCC CACTGGGCTCCT CCACCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	
5562	cg42346579	151	GCCGGTGTGGT CACAGCCCCACT GG[G/gap]CTCCT CCACCCGGGAC CTTTTGACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	

5563	cg42346579	204	GGGCTCTCCAGT GGAAGAGCGG AG[ <i>gap</i> ]CAGAG GCGGTGGTGGC AGTGGCTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	
5564	cg43916632	144	ATTTTACTCAA CAGTCTGCCTTT GATGTTTTCTT TCCATAAACAAA TAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15155 BET1P HOMOLOG - HOMO SAPIENS (HUMAN), 118 aa.	2.5E-58	7
5565	cg43961591	1282	CAGAGTGGTCT GTCAACGAGCTG G[ <i>gap</i> ]/G/ACGCTG TCACCAACGTGC AGTCCAG	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa.	3.1E-58	
5566	cg43997941	581	AGCTGGGTTAGA GAGAACTCAAAT TT/CJCTGATGGA AAACAAAACCGA ACAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O08612 SRC5H3 BINDING PROTEIN - MUS MUSCULUS (MOUSE), 494 aa (fragment).	3.6E-58	8
5567	cg43930685	1505	TCTTGAGACAGA CATTAGCTTTCT G/C/GJCTCCCTA TTCTCATAAGCA GCTAC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
5568	cg43930685	1506	CTTGAGACAGAC ATTAGCTTTCTG C/C/GJTTCCCTAT TCTCATAAGCAG CTACG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
5569	cg42466209	111	AGAGCCACCGG CAAGACAGCGTG ACIG[ <i>gap</i> ]CTGCT CACCTTCATCCT GCTGCTCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75827 DJ71L16.5 (KIAA0267 LIKE PUTATIVE NA(+)/H(+) EXCHANGER) - HOMO SAPIENS (HUMAN), 616 aa (fragment).	2.2E-57	

5570	cg43931116	257	ACAACAAAGATG GCCGTGATGAGT G[G/A]GTATAATA TATTTATATATAT ATAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5571	cg43931116	532	TAACACACACTT CTAAGCCACCTG T[G/A]ACCAACTT GGGAATTTCTGG CCCC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5572	cg43931116	543	TCTAAGCCACCT GTGACCAACTTG G[G/gap]AATTC TGGCCCTTGG GGACCACA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5573	cg43931116	553	CTGTGACCAACT TGGGAATTTCTG G[C/gap]CCCTTG GGGACCAACATCT CAGCCCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5574	cg43924285	1009	TGGGGTGATTCT TGCCCTTTTTTT [G/T]TTTTGTAAG AAAGAGGTTCCCT TCAT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5575	cg43924285	1172	AACTCTGTTTTT TAAATAAAAAA G[A/C]CTTACATG GTCAGGGATTGA TGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5576	cg43924285	219	ACAGCTCCTTAG AAGGCCAATAAT A[A/C]AGTTGGAA AAAAGGGAGTTT CCACG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15



5577	cg43924285	351	CACTGGGTAACCC TCCAGGCAGGA GC[C/gap]ACAGG CTGGAACAGGC GAACACTTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5578	cg43924285	674	TAAGCATTTCAGA CTTTAGAAATAA G[T/A]TTTTCATT TCAAACCTTTTATT ATAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5579	cg43924285	675	AAGCATTTCAGAC TTTTAGAATAAGT [T/A]TTTCATTC AACCTTTTATTAT AAC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5580	cg43924285	711	ACTTTTATTATA ACATGAGCTAAA[ C/gap]TTTAAAGAA ACAAACCCTAGTC TTCTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5581	cg43964035	270	AGGTACACAAGA GTTTGTGACACA A[A/gap]TAAAATA AGAATACTTCAC ACACGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5582	cg43964035	275	CACAAGAGTTTG TCAGACAAATAA A[A/gap]TAAGAAT ACTTCACACACG TATCAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5583	cg43964035	278	AAGAGTTTGTCA GACAAATAAAAT A[A/gap]GAATAC TTCACACACGTA TCAACAC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5

5584	cg43964035	281	AGTTTGTGACAGAC AAATAAAATAAG A[A]gap]TACTTCA CACACGTATCAA CACCAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5585	cg43964035	310	TTACACACACGTA TCAACACCCATAC A[A]gap]GGCATT ATTCTTCACACA GTAACAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5586	cg44032150	279	CCTGAGGTCCTA AAACGATTGCAG A[G]gap]CCTTGG GGTGCCCGGTG CGGCTGCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5587	cg44032150	713	TCTGTGTGTGAC AGAAGAGATTTT A[A]CJACACAGTG TGGGAAGTTTCT ATTTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5588	cg44032150	714	CTGTGTGTGACA GAAGAGATTTTA A[A]CJACACAGTG GGGAAGTTTCTA TTTTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5589	cg43982355	490	CATAGAAAACCT TGGAAAAAACCT T[C]TJTATAAAAC ACTGTTTCAATAT AATT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	
5590	cg43982355	500	TTTGGAAAAAAC TTTCTATAAAACA [C]gap]TGTTTCAA TATAATTTTATTA GCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	

5591	cg43982355	703	TCAAGAACTAGA AATGAAGTGCAC G[C/T]GTAGTGTC ACTTAAAGCAAA GCTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	
5592	cg43979919	118	CTCTATTTATATA TATATATATATA[ ap/T]AAAAGGTTTC TTTAGCAGTTAA ATAG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa.	1.2E-56	1
5593	cg43979919	122	TATTTATATATAT ATATATATAAAA[ A]gapJGGTTCTTT AGCAGTTAAATA GATTC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa.	1.2E-56	1
5594	cg43919432	204	GTTTGAAAAGTT CACTCTAAAGAA T[G/A]AAGTCACC TGTTGTCACGT CCTCC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
5595	cg43919432	281	TACCATCCTGTG GCTCCTTAAGGA G[G/T]CTTCTCTC TTTAATTCTCCAT GAGG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
5596	cg44928486	124	AACGTACATGGT TTAATACAACAA C[ap/A]AAAAAA ATTAATCAAGT GAAACGT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5597	cg44928486	131	ATGGTTTAATAC AACAAACAAAAA A[ap/A]TTTTAATC AAGTGAAACGTA ATAAAC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3

5598	cg44926486	77	ATAATTGCTCAC AAAGATTTCATAG A[ <u>gap</u> ]/TTTTTTTT TTATTGTTAAGCT GCAAC	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SU1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5599	cg44926486	86	CACAAAGATTCA TAGATTTTTTTTT gap/TJATTGTTAA GCTGCAACGTAC ATGGT	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SU1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5600	cg43991184	1164	AAACCATGTGGG TGCACAAAGCCA G[G/gap]CACTGC CAAGTGGAACAT GAGGTTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
5601	cg43968980	232	CGTTGCCCCCTC AGCCTCTAGGAG G[C/gap]CTCAGG ATTATGGCGTCC ATCTTAT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5602	cg43968980	262	GGATTATGGCGT CCATCTTATGAT A/T/CTGGCCAAA AGGAGACAGTCT TGGAG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5603	cg43968980	268	TGGCGTCCATCT TATGATATTGGC C[A/G]AAAGGAG ACAGTCTTGGAG GTGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5604	cg43968980	360	GGGAAAGGAATC TTTAGGCAGACT G[C/gap]CATCCA GGGACTGCTATT CTGTTCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5

5605	cg43968980	361	GGAAGGAATCT TTAGGCAGACTG C[C/gap]ATCCAG GGACTGCTATTG TGTCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5606	cg43968980	45	TTTTTTTTTTT TTTTTTTTTTT /TGTATTAGGG ATGCATTTTGAA TAT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5607	cg43968980	48	TTTTTTTTTTT TTTTTTTTTAGT /TTTTAGGGATG CATTTGAATATT TA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5608	cg43968980	49	TTTTTTTTTTT TTTTTTTTTAGT /AJTTAGGGATG ATTTGAATATT AT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5609	cg43968980	559	GGAGCAGGAG CTGAGGTGGAG ACG[G/gap]CCAC TGCCCTCTCTCAG CCTCTGTTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5610	cg43306180	951	AGCCACCCACCT CCAACACCTCCT G/ATJGCGTCTGA TGCTCCACCCAG GCCAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	
5611	cg43306180	959	ACCTCCAACACC TCCTGAGCGTCT G/ATJTGCTCCCA CCAGGCCAGCT CTCCTC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	

5612	cg43306180	960	CCTCCAACACCT CCTGAGCGTCTG ATTATGCTCCAC CAGGCCAGCTCT CCTCC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	
5613	cg44001479	864	TTTCCGCACCAA CGCGCCCGCCA TG[G/gap]CTGTG CCGACACCCAGAC CCCGAGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa.	1.4E-55	6
5614	cg44001479	295	CTGCAGATAAAA CCATCATCAGAA ATGTTTATTAAAT TAATTGCATATTT TGAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa.	1.4E-55	6
5615	cg43935092	599	CAGCCTGCTGTA CTGGCCATGCTG G[gap/G]CCAGCC CCACCTGGAGCT CAGTAAA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.8E-55	2
5616	cg44019498	366	AAAAGAAAGAAA GAAGAAATGGAAA ATGATAAAGAG AAAAAAACCACC ACAAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
5617	cg44019498	457	TGGTGAAGACTT TTGGTAGCAAAA TTC/TTGCACGGT TCTTAAATGGG AGTCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
5618	cg43917388	313	AAGAAAACTTT GTAATCAATATC CTT/CJGCTCATAA GTAAAAGTGGAA AAGAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa.	2.3E-55	1

5619	cg43917989	829	CGCCTTGCTGGT G TCTGAGCCCTGG G(G/A)CTCGGAC CACTGACCCCTGG CGCTTG	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.3E-55	11
5620	cg43928349	129	AAAAAGTGCTGC G TGCGGGCCGCAG AC[G/gap]CCAGT GCTGGCCCTCA GGGGGCCCC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5621	cg43928349	181	CAGCCGGCGAG C GGCGGGGACTT CCG[C/gap]CGCC AATCCCTGAGGG GGTAACATC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5622	cg43928349	182	AGCCGGCGAGG C GGCGGGGACTTC CGC[C/gap]GCCA ATCCCTGAGGG GGTAACATCG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5623	cg43928349	238	CAATCCCTGAGG C TGCGCAGGGTG GG[C/gap]CCCCG TCACCCCCCTGG GCTGCCCA	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5624	cg43928349	241	TCCCTGAGCTGG C GCAGGGTGGGC CC[C/gap]GCTCA CCCCCTGGGC TGCCCCACCC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	

5625	cg43928349	247	AGCTGGGCAGG GTGGGCCCCGC TCA[C/gap]CCCC CTGGGCTGCC ACCCGGGGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5626	cg43928349	252	GGCAGGGTGGG CCCCGCTCACCC CC[C/gap]TGGC TGCCACCCCG GGGTGTTCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5627	cg43928349	293	GGGGTGTCCC GCCGACTTCTGG GC[G/gap]GGGCC TCCCGGGCCAG GCCTGCCCG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5628	cg43928349	307	GACTTCTGGGCG GGGCTCCCCG GC[C/gap]AGGCC TGCCGGGGCG GGCCCCGAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5629	cg43928349	329	GGCCAGGCCCTG CCGGGGCGGG GCC[C/gap]GAGC AGCCGGACTGG CCAGGTTCAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5630	cg43928349	345	GGCGGGGCCCG AGCAGCCGGAC TGG[C/gap]CAGG TTCAGCGCGCCT CAGTAGGGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	



5631	cg43928349	415	GGACACCTGGG AGATGCGCGC GAG[G/gap]ACCG CCACAGCTTCCG CGCGAACTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5632	cg43928349	450	GCTTCCGCGC AACTGGCTGCTG CG[C/gap]ACCTC AGAGGGCTGCC CCGCGACCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5633	cg42904952	109	CCTTGAAGTGAT CTCTAGGCCCCA G[C/gap]CCCCAA TCCGCCACCAT CCGTGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	6E-55	
5634	cg43926664	28	TTTTTTTTTTTT TTTTTTTTTTAT /CJTTCACAAAGAT AATCTTTATTCAT A	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43805 NUCLEAR AUTOANTIGEN FO 14 KDA - HOMO SAPIENS (HUMAN), 119 aa.	9.8E-55	9
5635	cg43978709	487	GTAAGAAGATTTT ATTGTTCTATAG A/GCACTTCTGA AAAGAGATCTAA TTGA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa.	1.3E-54	
5636	cg43978709	582	TGAAGGCGTTAC AGCCCTCCTCTC C/A/GJAGGCTCA GGGCTGAGAAC GGTTAGC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa.	1.3E-54	
5637	cg43927929	216	GCCACAGCCTCC CGAGTAGCTGG GA/TCTACAGGT GCCCCGCCACCA CACCCAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Human), 354 aa.	1.6E-54	7

5638	cg43927929	417	TAAAGGACAGTC ATGTTGGCTCCA G[C/gap]CTAAGG CGGCATTTTCCG CCATCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Human), 354 aa.	1.6E-54	7
5639	cg41664708	437	TCACITTTACACG CTCATGGACTGA G[T/A]TTTACTC ACCTTTTATGAA AGCAC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2E-54	1
5640	cg41664708	446	ACGCTCATGGAC TGAGTTTATACT C[A/G]CCTTTTAT GAAAGCACTGCA TGAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2E-54	1
5641	cg43135067	688	GCCCCGGAGCC CCATCCTCGGCC TG[C/gap]CCTGG CTGGCCAGGAC CCCAGCGGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAAB3094 X11L2 - HOMO SAPIENS (HUMAN), 369 aa (fragment).	6.1E-54	19
5642	cg43983352	1027	GATTTGCAGCTG GTTCTCTCCAGGG A[A/G]TTGGCCC CGAAGCTGGCTC AGTTCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment).	6.9E-54	11
5643	cg43983352	1039	GTTCTCTCCAGGG AATTGGCCCGA A[G/gap]CTGGCT CAGTTCACCTCC AGGACCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment).	6.9E-54	11
5644	cg43123055	318	TAAGCCACGCTG TTGTGCTGCC C[gap/T]ATTATTG GTGTCATTTCTG CAGTAT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2

5645	cg43243118	170	GATATTATTGTG TTGACGCTGGT [C/T]CAAAATAAA TATTAGAAAGT TTTT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92599 MYELOBLAST KIAA0202 - HOMO SAPIENS (HUMAN), 508 aa (fragment).	9.9E-54	5
5646	cg43957121	174	TTAATGCTTTGG CAGATGAAGTAA C[G/A]TTTGAAAA CTGTTTGTGAAA ATAGT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa.	1.7E-53	4
5647	cg43957121	425	GCTTCCCAGACA GTCAAGGCCGG AG[G/gap]TCGCT CCTGTCCTGTGG TCTGACCC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa.	1.7E-53	4
5648	cg43946151	80	CATAAAGTGCAT CTTATTAAAAAT [G/A]TATAAAAC CACATAAATTCA GGGC	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62179 SEMAPHORIN C (SEM C) - MUS MUSCULUS (MOUSE), 782 aa (fragment).	2.3E-53	15
5649	cg43958224	284	TTGCTGTTTGT ACCGGGGCTCT GC[C/gap]CTGGT CCTGTCACCCCT GAGACGTC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19
5650	cg43958224	285	TGCTGTTTGT CCGGGGGCTCTG CC[C/gap]TGGTC CTGTCACCCCTG AGACGTCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19
5651	cg43958224	489	CAACACCCATTA GAAGCACCTGGA A[G/gap]GGGGGT TTTGGGAAACGG GCTCAGA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19

5652	cg43928097	224	TCTAACATTATT TATTCAGGTTT G/gapTTTTTTTT TGGCAACTATAA ATTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa.	4.3E-53	
5653	cg43969772	231	TAAATCATCATAA AAATGTTTAAAGT A/gapJAAAAAAA AAAAGAAAGAGA AAGAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5654	cg43969772	243	AAAATGTTTAAAG TAAAAA A/gapGAAAGA GAAAGAAAGA GGAGGTA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5655	cg43969772	243	AAAATGTTTAAAGT AAAAA A/gapA/GAAAGA GAAAGAAAGA GGAGGTA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5656	cg43969772	31	TTTTTTTTTT TTTTTTTTTTT /TTAACTAAAGG ACATTTATTATT TT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5657	cg43934126	297	GCATGGCCGCC ACGTGAGCTCAA AC/GTTCCGTTT ATTCAAAGCAG TAATAA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60372 R33683_3 - HOMO SAPIENS (HUMAN), 103 aa (fragment).	4.9E-53	
5658	cg43983169	953	GTTTATTGTGCA GAACAGACAGTG A/TAAATACACT AGAGAAATATTT TCAAG	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P52926 HIGH MOBILITY GROUP PROTEIN HMGI-C - Homo sapiens (Human), 109 aa.	7.7E-53	12

5659	cg43986294	1277	TGTGGTTTTTGT GTTTTTTTTTTT T/gap]CTTTTCC ATAGGAAAGAAT ATATA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa.	5.9E-52	
5660	cg43986294	1333	GTAATCCTAAT TCAAAGATGGCT C/A/GTGTGTGA GGGCATTGAGTT TGATT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa.	5.9E-52	
5661	cg43980016	384	TTTTTTTTTTT TTTTTTTTTTTTT G/CCTGCATAAAA TACTGTTTATTT G	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62509 ZINC FINGER PROTEIN - MUS MUSCULUS (MOUSE), 354 aa (fragment).	7.1E-52	1
5662	cg42732394	160	GTAGAGTTAAGG GCTTGGCAAGTT G/C/gap]CCACTC CTATCCCTGGTC TAGCTGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5663	cg42732394	243	TCACCTCCCTCC AGATTAGATGAG G/C/gap]CCAGCT GGCCTTTGGATG CCCCAGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5664	cg42732394	245	ACTCCCTTCCAG ATTAGATGAGGC C/C/gap]AGCTGG CCTTTGGATGCC CCAGGAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5665	cg44923668	377	AAACAAGCTTGG TCTCTTCTCTGC C/A/T]GGGTACCA CAGGGACACAC GCCAAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45963 ASPARTYL PROTEASE - HOMO SAPIENS (HUMAN), 518 aa.	1.2E-51	11

5666	cg43241808	1106	TTTCTCAACA TCTGCCACCTGA G[G/gap]CTAAGC CTACACACGGCG TGGCTGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	1.2E-51	
5667	cg43241808	137	ATTTTTCCTCA AATACTACACAT G/TTAAAGGAAC TGTTAAACTGAA AAAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	1.2E-51	
5668	cg43916927	392	AGCCATAAGTTA AAAAGAAGACAA G[C/gap]TGAAGC TACACACATGGC TGAIGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60829 JM27 PROTEIN, COMPLETE CDS (CLONE IMAGE 145745 AND IMAGE 257878) - HOMO SAPIENS (HUMAN), 102 aa.	1.9E-51	
5669	cg43980942	553	ATTGATTAACCT AAAAGGTGGACA IT/AJAATGTTTAT TTTAAATCTAATT GAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09132 SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) - Homo sapiens (Human), 144 aa.	3.9E-51	5 (5q21)
5670	cg44014613	277	AATAGCAGCAAA CTGGGAAAAAAA A[gap]/AJCCTCCT GTCCATAAATAG AAGTACC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa.	4.8E-51	1
5671	cg43994444	1045	GGACCTTGCACC ATCAGCTTTCTT G[G/A]GTTTCCAG CCTCCTGCCTCA CACTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa.	5.8E-51	
5672	cg43994444	460	GAAGGCAAGCTA GCAGGATGCTCC CTT/CIGAAACCTC TTTATTATGGG CCTTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa.	5.8E-51	

5673	cg43994384	449	GTACAAATAGAA ACCACAAAAGGG TTC/TJTGGAATTG GGTTAAGGTGAA GAGAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15553 PYRIN - HOMO SAPIENS (HUMAN), 781 aa.	8E-51	
5674	cg43999706	83	GTTTATTCAACA TTATGGCATGGC [C/gap]AGTGTA TTGTTCCAAACA AGGAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42973 PLECKSTRIN 2 - MUS MUSCULUS (MOUSE), 353 aa.	8.2E-51	14
5675	cg43916704	1031	CGTGGCAGGGG CAGCTATCTGGG AG[G/A]GCTAAAC AGCCTGGAGGC TGAGTCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5676	cg43916704	2091	TTGAAGCTGAGA GGCTGTGGATCT A/T/CJAGGAGATT CCAGCAGCATCA TGGCT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5677	cg43916704	386	CATCCAATTCCA GCATGGTCAGCA C[G/A]GAGATATT CACAGAAAGAAA CCCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5678	cg43916704	750	GAGCTTCCCAA TCCTAGAGAATG A/C/TJTGACTTA GAAAGTTTTGTT TTGTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5679	cg41004313	161	GGACAAAAGACA AAGAATGACACT T/TJCTCCTCTT TTGACTTTGACA CCCAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREBISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa.	2.5E-50	

5680	cg41004313	499	GTGGGGAGAAG CTTGAGGCTGG GGC[C/gap]TCCT CACCATCATCCT CCTCTTCCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa.	2.5E-50	
5681	cg42903672	129	AGGCGGCGGGG TGGGCGGGGGG AGC[C/gap]GAGC AGTCACGTATGG GGCATCTGC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34131 CGI-136 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa.	3.5E-50	
5682	cg43258766	157	CCTGCGTGCCTC CCTGCCAGTCTT C[C/T]CCGTCTAA CCCTCAGTCCCT CTATC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5683	cg43258766	353	AGCAAAACAGTCC ATGCCATCCAGC CT[C]GGGAGGC TGGGGGAGAGG AAGATGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5684	cg43258766	405	GGTGACTCCAGC ACAGCCAGCCTT G[C/gap]TCCGCA GGTGCCAGAGG CATAGGGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5685	cg43258766	409	ACTCCAGCACAG CCAGCCTTGCTG C[G/A]CAGGTGC CAGAGGCATAG GGAGGAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5686	cg41568177	62	GAGAAGACATT TATTGTTCTGG G[gap/G]TCTCTG GAGGCCCATG GTGGGGCT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa.	4.5E-50	1 (1q21)



5687	cg40357240	113	AGAGTGAATTT TTCTTGGGACT TTC/GTTTTTCTC CAGGGAAGGCT AAAAA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment).	5.4E-50	
5688	cg44010855	1541	CATGTTCTTTC CCTCACCACAAC AIG/TAACATGCA GTACTAAAGCAA TATAT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
5689	cg44010855	1749	GCTATGTACATG TCAGAAACCAAT A[G/gap]CATTGC ATGCAGGTTTCA TATTCTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
5690	cg43916819	497	AAGGCATACAAC ATGAGCCTTGTG G[G/gap]CACTGC CTCACCAACCAC TGGTGGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43182 DJ681N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	6.1E-50	20
5691	cg43970748	326	ATAGGGGAAGAC AACAGGCCAAG GC[C/gap]ACTCT GTGTTACTTTTC CTGAAGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7
5692	cg43970748	385	TTGAGGCACACA CTGGGGCCTGC AG[G/gap]CATCG AGTGAGCCGCG TGGAGGAAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7
5693	cg43970748	773	TGGCAGTGGCC ACTCAGGGCTTG GC[C/gap]ACAGG CAGGGCTTGGCT CAGTATCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7

5694	cg43279836	464	TGAGATTTCATAT TAAAAAGCCAC CIA/GIACATGATCA TCTGAGAAACCA ACACA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O77836 UDP-GLCNAC:A-1,3-D- MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4- N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	7.4E-50	
5695	cg43979181	139	TTGGGAGCAGCT GGGATGATGGG GA[C/gap]CCAC ATCCATAGGGCT GGGAGGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P02818 OSTEOCALCIN PRECURSOR (GAMMA- CARBOXYGLUTAMIC ACID- CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP) - Homo sapiens (Human), 100 aa.	7.4E-50	
5696	cg43298242	37	GGACAAGCCTTG CTTTATTGGGA A[G/T]GGATGGG ATCACAAATAAT CTCTGC	G	T				SILENT- NONCODI NG	water_ch annel	Human Gene SWISSPROT-ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.3E-163	
5697	cg42913771	348	CATGAGGTGTCTG ACTTCCAGCCAC G[T/C]AGATGCC GATTGCTTCCTG TGIGTC	T	C	Val	Ala (7868)		CONSER VATIVE	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
5698	cg43277632	1853	AACTACAGATGG TACACCTACATC TIG[C]TGCAGGA AGTGGCTCCCCA CACTGG	G	C	Val	Leu (7869)		CONSER VATIVE	ATPase_ associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3 )

5699	cg43931944	323	GCACTGGTAAAC CCCTCTCTGTAG A/G/CJCTTGGTCC TGGCATTATGGG AGCCA	G	C	Glu	Asp (7870)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5700	cg43931944	324	CACTGGTAAACC CCTCTCTGTAGA G/C/GJTGGTCCT GGCATTATGGGA GCCAT	C	G	Leu	Val (7871)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5701	cg43931944	688	TTCACCATGGTG CAAGTATGGCCT GT/CJACGTCAAG TTCGACCTGTCA CTGAG	T	C	Val	Ala (7872)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5702	cg43251803	2946	TAGCAGGACACT GCCATCTGAATC TG/CJCTCGGTAC GCACCTCGTTTCA TGACT	G	C	Gln	Glu (7873)	CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
5703	cg43251803	3000	CATCCCAGGCG GCCCCGGCTCC CCA[G/C]GCGGC CCCCGCCCCCC ACGCGCGCCG	G	C	Leu	Val (7874)	CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
5704	cg43933735	444	TGGCATTATGCA GACTCCCTCAGG C/G/AJTTGCAGTC ATCCATCAGCAA TTGAC	G	A	Arg	His (7875)	CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.7E-90	

5705	cg43988460	1624	CCAGCCTCCAAC TGGTATCTTCAT TACJTCAACCCG ATCTCGGGTCAG CTGTC	A	C	Ile	Leu (7876)	CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P19022 NEURAL-CADHERIN PRECURSOR (N- CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0	18 (18q11.2)
5706	cg43985533	328	AATAATTACCTG ATGGAAGTCACC CIGAJCTTGCCG GATGTAACCAGC CACTTC	G	A	Ala	Val (7877)	CONSER VATIVE	cathepsin	Human Gene Similar to SWISSNEW- ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHESPIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa. Jcds:SWISSPROT-ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHESPIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa.	2E-52	7
5707	cg43980411	430	CTCTGCAATCAA TGCATCCACAGG GJAGJATTATTA CTGGAAGTGTC AATAA	A	G	Asn	Asp (7878)	CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
5708	cg43970982	2132	GGACCTCGGG AAGCGGAGGTG CCG[C/G]TGGTG CTCCTGGAGAAC GAGGCAGA	C	G	Ala	Gly (7879)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
5709	cg43970983	1219	GCGGGTCCTCA GTGGTGGGCC ACA[G/C]AACAG CAGGAGCTGGG CCCTGGGCA	G	C	Glu	Gln (7880)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
5710	cg43970983	1688	CTGTAACAGACC TGCAAGCCACCG A[G/C]GTGCCCG GGCAGCGGGTG CGAGTGT	G	C	Glu	Asp (7881)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)

5711	cg43970983	1669	TGTAACAGACCT GCAAGCCACCG AG[G/C]TGCCCG GGCAGCGGGTG CGAGTGTC	G	C	Val	Leu (7882)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
5712	cg43991318	4971	CCGGGAGACCC CGAGGGAATACT CTA/TJCCCGTG GGCTGGGTCAC GGGGGGCCG	A	T	Tyr	Phe (7883)	CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
5713	cg43991318	5053	GTTGCGGATCTT CTTGATGGCAGA CT/GTCTTTCATG AGGCTGAGTCG GTGGAT	T	G	Glu	Asp (7884)	CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
5714	cg43933757	1606	TCCAGTGGGG GTGGGAGATCCT GCJA/GJTGGAG AAACGACAGAAA GCACACA	A	G	Ile	Val (7885)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
5715	cg43084083	2416	TCTAACCCACCTG GGAAATTC AAGG C[G/A]TTGGCATT TCAAAACACTGGT ATATG	G	A	Val	Ile (7886)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa.	0	9 (9q34.1)
5716	cg43956185	955	AACATTTCTATAA GGGCTCCTACAT T[G/C]ATAACGTA CTCTCTCACCAG ATGGA	G	C	Gln	Glu (7887)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
5717	cg43956185	1003	GGATAATTTACTC ATCTGTCTCGAC A/C[G]TATATAAG CAITTTGTACTG TGCGC	C	G	Val	Leu (7888)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1

5718	cg43956185	591	ATATCCACGTTT ACACACAAATTC A[G/A]CTGATTCA CCTGTTCTCAAA TAAAG	G	A	Ala (7889)	Val (7889)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
5719	cg42542496	440	CGTGACTCCCAT GTCCTTCACAGC A[G/A]ACTGAGC CAGTGCCCGAGA GGTTCAC	G	A	Arg (7890)	Lys (7890)	CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-189	3 (3q26.3)
5720	cg43957094	2211	AGCTTGCCCTGA TAAAAAAGCACC A[G/C]CCGGCGG AGCGGCCGCGG AGCGACC	G	C	Leu (7891)	Val (7891)	CONSER VATIVE	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.9E-164	6
5721	cg43242733	635	GACTTGATGAGA ATGGAAAAGATT G[C/T]AATGGAGA AGGTGIGTTGGA AAGTC	C	T	Ala (7892)	Val (7892)	CONSER VATIVE	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.3E-154	5
5722	cg43986855	3915	AAGTTCTCCGGG TTAGGCCCACTTC A[G/C]TGGGTCAT GATTCACAGACC ACTGG	G	C	Leu (7893)	Val (7893)	CONSER VATIVE	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
5723	cg43966704	1275	CGGCCCTCAAA CCCGATGCTTG A[T/C]CTGCCCA GGATCCAGTCG GGCCCC	T	C	Ile (7894)	Val (7894)	CONSER VATIVE	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11

5724	cg43966704	596	GAGGTGTCCCA GCCGCCGTGA CA/C/A/C/C/CAG CATGCTTCTCAA TCAGTTC	A	Gly	Val (7895)	CONSER VATIVE	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
5725	cg43962888	447	GCAGGGGACTG GGTTGGAGAGG GAG/A/G/T/CATG CTGGCTGCAAAG AAGGGACT	G	Ile	Val (7896)	CONSER VATIVE	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5726	cg43962888	463	GAGAGGGAGAT CATGCTGGCTGC AA/A/G/GAAGGG ACTGGACCCATA CAATGTA	G	Lys	Arg (7897)	CONSER VATIVE	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5727	cg43962888	517	GCCCCAAAGGG AGCTTCAGGCAC CA/G/A/GGAAGA CCCTAATTAGT CCCCGCC	A	Arg	Lys (7898)	CONSER VATIVE	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5728	cg43962888	546	AGACCCCTAATT AGTCCCCTCCAT CT/A/C/CAACAAG AGAATAGTAGGC TGCAT	A	Ser	Thr (7899)	CONSER VATIVE	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5729	cg43962888	621	CGTCTGGTTTGG GCTGCACAAAGG C/G/C/JAGGCCCA GCGATGCCCCCG GCTGTGG	C	Glu	Gln (7900)	CONSER VATIVE	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5730	cg34396112	3497	ACTTGCTTCCCA GCAAACCAAGCG CA/G/C/CTGCTC CAGGACCCCTCT GAACACC	C	Leu	Val (7901)	CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)

5731	cg44033747	1337	TTGGCGAATATG GCTGCCATGTT G/GCJAATCTACC ATGGTTCCCATG GGCTG	G	C	Gly	Ala (7902)	CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
5732	cg43057018	1597	TGACCTAATGAA CCAAAGGAAAAG C/GJTCGGAACA ATCCTCATCTTT GAAG	A	G	Ile	Val (7903)	CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.jpds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
5733	cg43973273	1476	CAGCCTTCTCTT GGACAGCGACAT A/C/GJATCCCTTT CTGGGGCATGA GTTTTC	C	G	Val	Leu (7904)	CONSER VATIVE	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment).	2E-112	
5734	cg43327854	1114	TCAAAGTGGAGGA TGATGGGGATG GC/GAJATTACAT GTCTGAGCCTGA GGCTGT	G	A	Asp	Asn (7905)	CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
5735	cg43958856	566	AACCGGCATGG CCAAAGCCCGC GCG/A/GJTCGGC ATCGACCTGGGC ACCACCTA	A	G	Ile	Val (7906)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0	6
5736	cg44017749	12288	GCGCCTCCTACC ACTTCCAACCGC C/GAJCCGGCGA CAGATTGACCGG GGTGTC	G	A	Arg	His (7907)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12



5737	cg43950268	2136	GCTCCCGGCTG AGGTTACAGGG AATG/CJTCCTCA CTGTCCACCACA CCTCGGA	G	C	Asp	Glu (7908)	CONSER VATIVE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
5738	cg43982507	637	CATGGGCACGTC CGCGCTCTGGG CGC/GJCTGGC TGCTGCTCGCGC TGIGCTG	C	G	Leu	Val (7909)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
5739	cg43949555	1239	AATCTGATGGAT GACATAGAAAAGG G/C/TAAGTAGAC GATGGTGTTAAT ACTTTC	C	T	Ala	Val (7910)	CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCUS SP. (STRAIN SY), 545 aa. lpcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
5740	cg44011461	2430	GATGAGGGCATA GATGCTGCTGAA G/C/JTGAGGTT GTCAGTCAAGTA GTATTT	G	C	Thr	Ser (7911)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0	16 (16q24.1)
5741	cg43942273	1775	CCTCAGGGGTC CAAGAGGCGGC TTG/CJCAAAAG GGATTCCAGGA AAATGGC	G	C	Ala	Gly (7912)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16

5742	cg43942273	335	TACTTCTTTGTC CTTCAGCTTCTG G[G/C]CCGCCTG GGTGTGGCACC AATCTG	G	C	Ala	Gly (7913)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16
5743	cg43957743	1066	TGGCATACCTGG ATATTTTAATCCA [G/C]TGGAGATAA AAGACAGCCCAC TAGG	G	C	Thr	Ser (7914)	CONSER VATIVE	esterase	Human Gene SWISSNEW-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). pcls:SWISSPROT-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.9E-178	
5744	cg43286057	1921	GGACCCAGCAG GACGGGATATCT CC[A/C]TCCGCC CTCTCCTGGAGC ACTGTGA	A	C	Ile	Leu (7915)	CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
5745	cg43286057	1925	CCAGCAGGACG GGATATCTCCAT CC[G/A]CCCTCTC CTGGAGCACTGT GAGAAC	G	A	Arg	His (7916)	CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9

5746	cg43969014	618	GTCTGCTGCGTA GGTGGAGTTGGT C[A/C]CAAAGGTC ACAGGCTGGGA GGGGTC	A	C	Val	Gly (7917)	CONSER VATIVE	glucuronidase	Human Gene Similar to SWISSPROT-ID: P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.4E-80	5
5747	cg43943531	2148	TTTGAGCTTGAT GTCCTGGAGGAA G[C/G]ATATACCA CAGAACATTGGC TGGTC	C	G	Ala	Gly (7918)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0 (11q23.3)	11
5748	cg43943531	915	GTCCTTTTCATCA GAGCACATGGCA G[C/G]CTTTGGG GTCCTTGGTCTC TGCCAG	C	G	Ala	Gly (7919)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0 (11q23.3)	11
5749	cg43065549	1676	GGTCAGAGCAGT CAAGGAGGGGA CG[C/G]TGGGGC TGACCCCGAGCAG TGTCAGA	C	G	Leu	Val (7920)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0 (15q15)	15
5750	cg44034764	282	CTCGGAGGTGT GGAGGGCTGTG AGT[G/T]TCGTGA GAGTCCTGGGG GCTGGGCT	G	T	Asp	Glu (7921)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0 (Xp21.2)	7
5751	cg44004239	177	GACACCAGAGG GGCTTAGGCTTC TT[G/C]ATCCACA GCAGAGTTTCT GGGATT	G	C	Gln	Glu (7922)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
5752	cg43094362	292	AGACGTGGACCA CTGGCTCACGAC A[C/T]GAGGCTG CCTCCTGGAATG GCTTGG	C	T	Arg	His (7923)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID: P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7

5753	cg43987514	964	TAGCGCAGAGA GTTCTGTGCGCG CTGIC/GITTCGG CTGGCCCCCAGT GCCCCAGG	C	G	Ser	Thr (7924)	CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
5754	cg43958628	520	TATTACTTAATTG GTGAAAAAATTG C/TATATTGTGAA CTTAAAGGATCA GTA	C	T	Ala	Val (7925)	CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	8.6E-206	
5755	cg43059879	369	ACCACAGTGGCT TTTTTCACAGGT A/A/CJTITACAA ATGCTTTACAA TTGGC	A	C	Leu	Val (7926)	CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jpdis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jpdis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	6.6E-199 (17q23)	
5756	cg42845511	1726	AAGATCTCGTAC GCTCAGTATGAG A/A/GJTACCTGA AGTCAGACAACA TGATC	A	G	Lys	Arg (7927)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	2.9E-86 (20q12)	
5757	cg43054905	1258	GTAGTCATAACC ATCCACATTAAAC C/G/AJCCGGCAT AACATAGAAATC CACAAG	G	A	Ala	Val (7928)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85 (13q14.1 1)	

5758	cg44021513	1357	TCTGGCCCTGCT GGTACGCGGG GCIG/CJTCTGCG CTCCTGCTGAAC TTCACTC	G	C	Asp	Glu (7929)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
5759	cg43965366	1819	TCITTTAAAGGA TTGGTAACTGA AIC/TJTGTCACAG TCATGTCAGAAC CAACT	C	T	Val	Ile (7930)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)
5760	cg42713500	1094	GAGGCCCGAGG CCGGGCCCTGC AGG[C/G]CGCG TAGCCAAACGAC GAGTGCTG	C	G	Gly	Ala (7931)	CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:P78337 PITUITARY HOMEOBOX 1 (HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT) - HOMO SAPIENS (HUMAN), 314 aa.   pcis:SPTREMBL- ID:P78337 HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT - HOMO SAPIENS (HUMAN), 314 aa.	2.5E-174	
5761	cg43928699	378	GGTGAACGACTA CACGCACGCCCT C[C/G]TCCGCCA CGACCCCTGG GCAAACC	C	G	Leu	Val (7932)	CONSER VATIVE	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.8E-148	10
5762	cg42908326	924	AGCAGCCGCCA AGACCACCAGCA AG[A/G]ACTCCA GCATCGCCGATC TCAGACT	A	G	Asn	Asp (7933)	CONSER VATIVE	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEOBOX PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
5763	cg43285385	434	TTCAATTAACAAAA AACTCTGCTAAA T/AJAAAATGCGG TTTTCACAGCAT TAGG	T	A	Tyr	Phe (7934)	CONSER VATIVE	hydrolas e	Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.8E-173	8

5764	cg43929210	956	ACTGGTTTGGCA AAACGAGCCTTA A/C/TJTGCCCTTGA ATCTTGACACAT CATT A	C	T	Val	Ile (7935)	CONSER VATIVE	hydroxyst eroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0	5
5765	cg44014662	1207	TCTCGAGCAAGA CGTTCAGTCCTG T/C/TJCATATA GTCCATGAGGAA TAAAC	C	T	Asp	Asn (7936)	CONSER VATIVE	hypoxanthine	Human Gene Homologous to SWISSPROT-ID:P00492 HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) - HOMO SAPIENS (HUMAN), 217 aa.	9.1E-115 X (Xq26)	
5766	cg43925670	312	TTTAGAAGAAA AAGTCTGGTGAA GT/AJTCCATAC TTGAATCAGGAT TGAGT	T	A	Thr	Ser (7937)	CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 . aa. Idcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
5767	cg42862121	1623	TCATGTGGGG CCAGACTGCAC GC/A/CJTCTGTGA GGCTCAGGCTTG GCAACA	A	C	Asp	Glu (7938)	CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q13568 INTERFERON REGULATORY FACTOR 5 (IRF-5) - HOMO SAPIENS (HUMAN), 504 aa.	4.2E-284	7
5768	cg43510640	257	GCCTGGACGAC CAACACTGGGAT GAT/CJGATGAG CAGAATGGTCAT GAAGATG	T	C	Ile	Val (7939)	CONSER VATIVE	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.2E-62	

5769	cg44339782	257	GCCTGGACGAC CAACACTGGGAT GA[T]CGATGAG CAGAATGGTCAT GAAGATG	T	C	Ile	Val (7940)	CONSER VATIVE	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.2E-62	
5770	cg43951261	4481	TTTTACCCAGGC AAATCAAAAGCC A[C]G[T]CCAGAAA AATCTTTGCATG ACAAA	C	G	Thr	Ser (7941)	CONSER VATIVE	isomeras e	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0	3 (3p)
5771	cg43989064	841	AATGCTTTGGTA TTTGATGGGTCT A[G]T[T]CAAGAG CCTCTAAACAAC TGTC A	G	T	Leu	Ile (7942)	CONSER VATIVE	isomeras e	Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP- 40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa.	1.3E-200	4
5772	cg44001328	901	GGGGTTGAAATA GCGCAGCAGCA CT[G]A[CG]TTCCA AGTCTTGCTGCTG CTGGCA	G	A	Ala	Val (7943)	CONSER VATIVE	isomeras e	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. lpcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
5773	cg43961450	1230	TCAGACTCAAGT CCAAGTCCTTTA A[G]T[C]AGCAGT GCGTAGAACTGG GGTCT	G	T	Leu	Ile (7944)	CONSER VATIVE	isomeras e	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-) - RATTUS NORVEGICUS (RAT), 361 aa.	1.8E-117	5

5774	cg43145505	314	AGAATGCCTCCG TGAGGCTACATT A/A/GTAAACCAT AAGCATGAACCTA TTTAA	A	G	Ile	Val (7945)	CONSER VATIVE	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.   pcsl:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0	3
5775	cg43019995	1904	CCCCCAAACCTGC CCCCCGAGCTTC TTTAAJCCCCCATCA CCGTGCGCTGTT GCGAT	T	A	Phe	Tyr (7946)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa.	0 (7q11.23)	7
5776	cg43947829	1855	ACAAGCTTTTGT GCTTGCAAAGGA A/C/TJGCGCTGG GAAGAATTGAA GGACAC	C	T	Val	Ile (7947)	CONSER VATIVE	kinase	Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
5777	cg43917871	1684	CCCAAGATATCA TTGAAACGTGGA TIC/TJTAATTCAA TGTTGTATTTGT CAATA	C	T	Asp	Asn (7948)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215 (20p13)	11
5778	cg43981459	1050	ATTGTTTCCTGG TACAGACCATAT TIG/AJATCAGTTG AAGCTCATTTTA AGACT	G	A	Asp	Asn (7949)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:Q16539 MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.-) (MAP KINASE P38) (CYTOKINE SUPPRESSIVE ANTI- INFLAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2) - HOMO SAPIENS (HUMAN), 360 aa.	3.1E-194	6



5779	cg43987006	452	GGAGAACTTGAG GGGGCTGACGG GG[G/A]CCCGGG GGCTACTGTTGA GGCGCCT	G	A	Ala (7950)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S6 KINASE I (EC 2.7.1.-) (S6K) (P70-S6K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa.	3.1E-176	11
5780	cg44918533	870	GGACTGCAAGTA GGTGGAGCACA CA[G/A]CCTTGGA GACGTGGCTGG CTGAACC	G	A	Val (7951)	CONSER VATIVE	kinase	Human Gene Similar to SPTREMBL- ID:Q19632 SIMILAR TO SERINE/THREONINE PROTEIN KINASE. NCBI GI: 1086650 - CAENORHABDITIS ELEGANS, 821 aa.	1.2E-70	
5781	cg43991478	1274	CTTTTCAAATAG CGCTTGTTGGAAA [A/G]CAGTAGGT CCGACGGCCCGG TGAGTC	A	G	Ala (7952)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5782	cg43991478	1275	TTTTTCAAATAGC GCTTGTTGGAAAA [C/T]AGTAGGTCC GACGGCCCGGTG AGTCC	C	T	Ile (7953)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5783	cg43991478	1341	ACGTCAGCAAGA TTGTGGGGCTGC A[G/C]CCGGGTG AGGTCACGCAG GATGGTG	G	C	Val (7954)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5784	cg43920644	1423	GTTCTGCAGGCG CTGCCCATGTGCG A[T/G]CATCTTGA TGACATCATCAG CAGAG	T	G	Leu (7955)	CONSER VATIVE	kinesin	Human Gene SPTREMBL-ID:Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa.	0	1
5785	cg42918454	2315	CAGATGCAGCTG AGCCTGGCAGAA A[G/C]TGAAGCTT CCTTGGGAAACA CTAAC	G	C	Thr (7956)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0	1

5786	cg43983535	4190	TCAACAGCCTCC TTCTTTTCTCCA [C/A]TGCAGTCAT GTTTTCTGATTT ACT	C	A	Val	Leu (7957)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
5787	cg42536982	7508	TCTGCATTGAGC GTTCTAATGCGT T[G/C]CAAGCGA AGGCGAATATAT CGTGCA	G	C	Gln	Glu (7958)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa.	0	
5788	cg42930646	1216	CGTCAATGTTAC TGATGCGGATAG C[G/C]TATGGATG GAAATGGACGAT GAGGA	G	C	Val	Leu (7959)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa.	1.8E-198	1
5789	cg43966144	718	AAGCTTGTCATG CCTCACAGCAGT G[C/T]GCACAAG ACTGCCCCAGCCC AATGGA	C	T	Ala	Val (7960)	CONSER VATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.1E-147	6 (6p21.3)
5790	cg43111577	1089	GCTTATGAAGAA GAGAACAAAGCT G[G/T]GGAGAAG ATGCCAGAGAG CTGTCC	G	T	Gly	Val (7961)	CONSER VATIVE	misc_cha nnel	Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
5791	cg44019843	483	GCCAGACCATCT CTGTGCACCCCTG G[T/C]GCCCTCTG GGCCCTGAGTG CTTGCGC	T	C	Val	Ala (7962)	CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0	17 (17q23.1)
5792	cg40367355	1058	CGGATTCCTCTC AACCAAGCCACT G[C/T]CAAAATTC ACGTGGACTCCT CCTCT	C	T	Ala	Val (7963)	CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.1E-199	21

5793	cg44929972	1149	GTGACTTTTITTA TGAAGACATGGA [G/T]TCCTTGACG CAGATGCTTAGG GCCT	G	T	Glu	Asp (7964)	CONSER VATIVE	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
5794	cg43979114	287	CCTGCAGGACAC ACCATCCCCCAA GT/C]CCACTGG ACTAAACTCAG CATTCC	T	C	Val	Ala (7965)	CONSER VATIVE	ngf	Human Gene Homologous to TREMBLNEW-ID:G387171 NERVE GROWTH FACTOR - MUS MUSCULUS (MOUSE), 307 aa.	1.5E-130	1 (1p13.1)
5795	cg43924936	3009	CTCTTACTTCA GCCTCCTCTTCT TIG/C]CAATTTCT TTTTCGTTGCAA TGTC	G	C	Gln	Glu (7966)	CONSER VATIVE	nud_rec pt	Human Gene TREMBLNEW- ID:G2655006 THYROID HORMONE RECEPTOR COACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 920 aa.	0	5
5796	cg30421838	2486	GCCAGCGCCTTT GCCCCGCCGCG GA[G/C]TTCACCC TGTGCTCGTGCC ACCCCG	G	C	Glu	Asp (7967)	CONSER VATIVE	nud_rec pt	Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. [pcis:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
5797	cg43315956	2799	ACTTTCCCTTCA CTCTGCCAGCTG G[G/C]TAAATACA CCACGAAATCCA GTGCT	G	C	Gly	Ala (7968)	CONSER VATIVE	nud_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
5798	cg43315956	3542	CAGTGGGTCA GTCAGTCACCCAC TC[G/C]TGCAATA AGACATTTTCTA GCTACT	G	C	Val	Leu (7969)	CONSER VATIVE	nud_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
5799	cg43972383	1195	ATCTCTCTAAAT AATGAAACTTGA A/C]AATGAAAT AAAGCCTTGGAT AGCC	A	C	Glu	Asp (7970)	CONSER VATIVE	nuclease	Human Gene Homologous to SWISSPROT-ID:P12753 DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1312 aa.	1.6E-149	5

5800	cg43947341	270	CCAACTCCTTGG GTTCTTTCCCAG A/G/C]CTCTTACT TTCTGAGGGCCC AGGCC	G	C	Ala	Gly (7971)	CONSER VATIVE	nuclease	Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa.	1.1E-115	
5801	cg43951535	1535	GGTGAACACAG CGAGTAGCTTTT A/G/C]CCCTTTGC TTGGGCAAAACCT GCTGA	G	C	Ser	Thr (7972)	CONSER VATIVE	nuclease nhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)
5802	cg44012756	2324	ACCTGCAAAAGAC ATGACCAGTGGC T/A]TCGTGTGCA CCTGCCGGGAG GGCTTC	A	T	Tyr	Phe (7973)	CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
5803	cg43297056	2389	CACTGCTTCCCC AGCCGGCCCTTC A/C]G]GCGCTTG GCAATCAGTGTG CACTGC	C	G	Val	Leu (7974)	CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103	20 (20q13.1 )
5804	cg42849556	1051	CTCCTAGTTCC AAAGCCCTTGA A/G/A]ACCCAG CTGTCACCCAGGC CAGAAA	G	A	Arg	Lys (7975)	CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.8E-287	1 (1q25)
5805	cg43999400	1236	GATGTGACATGG GCAACACAAGAA A/A]G]AATTTCTT TGCAGTGGCTCA GGAGG	A	G	Lys	Arg (7976)	CONSER VATIVE	peptidas e	Human Gene SWISSPROT-ID:P27487 DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN- 2) (ADABP) - HOMO SAPIENS (HUMAN), 766 aa.	0	2 (2q23)
5806	cg41626506	634	AGCCAGCGACAT GGAGATCCAAGT C/A]G]CCCGAGG GAGCCTCCCGG AGTCTAC	A	G	Val	Ala (7977)	CONSER VATIVE	peroxida se	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0	3 (3q26.3)

5807	cg42691989	825	CCGGGTGGTTGT GCCTCAGAGCG AA/GC/CACATT CTCAATCAGCAC GGCCCT	G	C	Ala	Gly (7978)	CONSER VATIVE	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101	14 (14q24.1)
5808	cg43956369	5054	AGTTGAGCAAAA TTGGACACACCG GT/AJACCTCGTT CTGACTGAGTTA CACAG	T	A	Thr	Ser (7979)	CONSER VATIVE	phosphatase	Human Gene SWISSNEW-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R- PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.   pcis:SWISSPROT- ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.	0	6
5809	cg43321833	2339	CTCACGTTCCACC ATCAATCTCCTG G/G/JGGTGATG CTCACCATCAAA AGGAGA	G	T	Gly	Val (7980)	CONSER VATIVE	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
5810	cg43956187	390	TACAGTAATAGA TTTTGGAGGAT G/A/GJATGGGA GTATAATGTTGT GATCAT	A	G	Ile	Val (7981)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q05209 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa.	0	7 (7q11.23)
5811	cg36899343	3058	TGTTGGAGGCCG CAAATCTGCATT TJG/AJATCCCTG CAGCTGAAGGCT TTCCC	G	A	Asp	Asn (7982)	CONSER VATIVE	phosphatase	Human Gene SPTREMBL-ID:Q13187 INOSITOL POLYPHOSPHATE 4- PHOSPHATASE - HOMO SAPIENS (HUMAN), 938 aa.	0	

5812	cg43928335	3498	CAGCAAGAGCTA ATAGTACCTCAT CTTATCATCATATA AATTGTATCTGT AAGAA	A	Glu	Asp (7983)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.2E-302	11 (11q22)
5813	cg43984117	823	GGTGACGTCAG GCCCAAACACTGAC AGG/CJTCACGC CCCGCTTGCTGA TCGAGCG	C	Thr	Ser (7984)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.1E-273	
5814	cg43988365	2812	ACAGTGCAAGGC CATGAAGTGCGG CTT/CJTGCTGTG TGCACGACCTGG TAAAA	C	Lys	Arg (7985)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa. lpcis:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
5815	cg42688448	1803	GGTTCAGGAC GAGGCGCCCATG GTA[G/C]TCTGAG GCTGGGCATGG GCATGGGC	C	Thr	Ser (7986)	CONSER VATIVE	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
5816	cg43968623	836	GGCACCATTGAA GTGTCAAAGGTG G[G/T]ACGGGG ACTGTCCTGGCT GTGTGG	T	Gly	Val (7987)	CONSER VATIVE	polymerase	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
5817	cg42937321	354	GCGCGTGGTCAT CAACATCTCCGG G[C/G]TGCGCTT CGAGACGCAGC TGAAGAC	G	Leu	Val (7988)	CONSER VATIVE	potassium channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.4E-284	1 (1p21)

5818	cg43331104	330	GCGCGTGGTGA TCAACATCTCCG GG[G/C]TGGCT TCGAGACGCAG CTCAAGAC	G	C	Val	Leu (7989)	CONSER VATIVE	potassiu m_chann el	Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1) - HOMO SAPIENS (HUMAN), 495 aa.	5.6E-266	12
5819	cg43262191	773	GGCTTTCGGGTA CCTGCTGGGCTC T[G/A]TCATGCTG CAGATCTTTGTG GACTA	G	A	Val	Ile (7990)	CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0	3
5820	cg43923853	1874	TGGAGTATGCAT ACAAGAAGTCGG C[C/A]TCCACTGG TATTTATGACAC GCCA	C	A	Glu	Asp (7991)	CONSER VATIVE	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.lpcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2E-149	4

5821	cg42918089	408	CCTATAACTGGA ATGTTAACTCC C[G/A]CGTCATAG AAATAATGCAGA AGCCC	G	A	Arg	His (7992)	CONSER VATIVE	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.   pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.4E-146	11 (11q21)
5822	cg43310246	1169	GCAAGACAGTG GATGGCCCCCG GGA[G/C]GTCAC GCTGCAGGCCAT GGCCGATG	G	C	Glu	Asp (7993)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa.	1.1E-141	20 (20p11.2)
5823	cg43310246	1170	CAAGACAGTGGA TGGGCCCGCGG AG[G/C]TCACGC TGCAGGCCATG GCCGATGG	G	C	Val	Leu (7994)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa.	1.1E-141	20 (20p11.2)



5824	cg43074055	536	CGACGCGGAGA ACAAACTGAACG AC/A/GJTTCCT CATCCAGCTGAG CAGCCC	A	G	Ile	Val (7995)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.7E-138	19 (19p13.3 )
5825	cg42309989	317	GTTAAGCCTT ACTGACTGACTG A/G/A/CTATAGGC GAGGTGAAGGC TGGTCC	G	A	Ala	Val (7996)	CONSER VATIVE	protease	Human Gene Similar to SWISSNEW- ID:P31795 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment). pcIs:SWISSPROT- ID:P31795 POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment).	8.3E-82	
5826	cg43979831	1345	GGCACCAGGCG TGCAGCAGCCAC CA/G/C/CTTCGC GATCAAATTCTT CTCTGCC	G	C	Ser	Thr (7997)	CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.1E-228	14
5827	cg43268468	1183	CGGTGAATGATG GATTCTGTTCCG TIG/C/CTCCGCTC CCAGCGAGAGG GCCGAG	G	C	Gln	Glu (7998)	CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3 )
5828	cg43268468	1184	GGTGAATGATGG ATTCTGTTCCGT G/C/GJTCGGCTC CCAGCGAGAGG GCCGAGA	C	G	Glu	Asp (7999)	CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3 )

5829	cg43268468	286	GCCCCTGTGTCT GTGTCCCTCAGT A[C]TGAAGATGA AAGGCTGGTTAA GGTGA	C	T	Val	Ile (8000)	CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3 )
5830	cg43060292	907	AGGGAAAGTTGT GGGTCTAATTCA A[A]GJACCTCAAG CCAAACACCATC ATGGT	A	G	Asn	Asp (8001)	CONSER VATIVE	protease nhib	Human Gene Similar to SWISSPROT- ID:P09006 CONTRAPSIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa.	2.2E-83	X (Xq22.2)
5831	cg43938319	6705	CAACAAGTATGG GGTCAGCCTCAT C[G]AJATCCCAA ACGAAGGATATC CTCAC	G	A	Asp	Asn (8002)	CONSER VATIVE	struct	Human Gene SP TREMBL-ID:Q13402 MYOSIN VIA - HOMO SAPIENS (HUMAN), 2215 aa.	0	11 (11q13.5 )
5832	cg44033566	3186	GGACTCGCACC CTGAGCAGAAG GAG[A]GJATATTG GTCAGCGGCAAA AACACTT	A	G	Asn	Asp (8003)	CONSER VATIVE	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.   pcds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
5833	cg43957486	2089	ATCTGCGGGCC CGACTCGGCCCT TG[C]TCGGCCA CATTGGCACCGA CTGTGAC	C	T	Ala	Val (8004)	CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0	20 (20p11.2 )
5834	cg43916919	230	AAATTGCTTGAA GATGGGACTCTC A[C]TGGCCCTG AGGCAGAAATCTC CACCTG	C	T	Arg	His (8005)	CONSER VATIVE	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.   pcds:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)

5835	cg43918346	706	GTGGCACCCGCC GGGATGGAAAGT GGC/GJAGAATG TTCATTTTCATCG CTCGGG	C	G	Gln	Glu (8006)	CONSER VATIVE	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.4E-130	
5836	cg43973395	262	AGCAGCCGGAA GAGGAGGCTGC GGA/GCJGAGGA GGAGGAAGCCC CCGAAGAGC	G	C	Glu	Asp (8007)	CONSER VATIVE	struct	Human Gene Homologous to SWISSNEW-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa.pcls:SWISSPROT-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa.	2E-114	19 (19q13.4 )
5837	cg43961212	2158	GATCTGGAAGCC GGACATCCTCTG A/GCJCAAGTCG ACTGATCCGCTG GCGAAC	G	C	Ala	Gly (8008)	CONSER VATIVE	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.4E-114	7
5838	cg42522566	273	GGCCAGGTGCA CAGGTGTACAGA GA/GA/GTCTACA GGCCTTGCACTG GCAGCC	G	A	Arg	Lys (8009)	CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
5839	cg43977322	1441	CTTCGGGTCTCC AGCTGCAGGTTT TIG/CJCCCTCTCCA GCTGTAATTTGT GGTTC	G	C	Gln	Glu (8010)	CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.5E-52	16
5840	cg40388639	4912	ATTTTGGAGTC ACCCTGCGAACG TTA/TJCGAAGTGA CCAACCGCCTTA GATCT	A	T	Tyr	Phe (8011)	CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2 )

5841	cg43987111	1818	GGAGTCTGAGAA CTTCGTGTATTT GIC/GJCCACAAG GGCAATAGAGCA GGTCTC	C	G	Gly	Ala (8012)	CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
5842	cg43124627	1841	ATTATTCAAGA GCTGCCAAAGAC TJA/GJTCAGTGG GAAGACAAAAG AAATGA	A	G	Ile	Val (8013)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.7E-79	16
5843	cg43124627	846	ATCATGGCCATA TTCTTTACCAGT GIC/GJACAAGT GGATATCCGAAA ATGACT	G	C	Gly	Ala (8014)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.7E-79	16
5844	cg43933068	580	AGGTGGATGCC GAAGAAAAAGAA GAT/GJGTGAAAT CTTGTGCTGAGT GGGTGT	T	G	Asp	Glu (8015)	CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12

5845	cg42711317	1131	TAAAGATGTGGG ATTGAAAAAAGA A/G/A/TATATTGCA ATGTGGGAAGTA AATGA	G	A	Asp	Asn (8016)	CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q23)
5846	cg43278427	1120	CTTGATGTGTAA TGAGAGCAGTAT G/C/G/JAGAGCTT GCGCCAGAGAA AATCTGT	C	G	Gln	Glu (8017)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
5847	cg43278427	1124	ATGTGTAATGAG AGCAGTATGCAG A/G/C/CTTGCGC CAGAGAAATCT GTGAAT	G	C	Ser	Thr (8018)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
5848	cg43306266	315	CCTACACAGGCA TGTTGGCGCCCC GA/G/C/CGTTCC GCCGAGGCGCG GGGCAACC	G	C	Glu	Asp (8019)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.8E-212	1 (1p31.2)
5849	cg42704646	311	CCTACACAGGCA TGTTGGCGCCCC GA/G/C/CGTTCC GCCGAGGCGCG GGGCAACC	G	C	Glu	Asp (8020)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.1E-194	1 (1p31.2)
5850	cg2514276	646	TACGTCACCATC TTCTACGCCCTG G/G/C/JTACCAC CACATCATGACG GCGAGG	G	C	Gly	Ala (8021)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa.	7E-172	

5851	cg40245117	1509	TGCTCTGTCTATG GCTGCCCTTTATC TTA/CITCATCAAC TGCATCATCTAC TTTAA	A	C	Ile	Leu (8022)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa.	1.5E-167	1 (1p21)
5852	cg32423505	737	CACATCAGAAGG AAGACTACCAAT ATT/CJGGCAAAA CAAGCTTGAAAA GGCTA	T	C	Ile	Val (8023)	CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.2E-55	3 (3q21)
5853	cg43335562	339	CAAGACCTAGCT CCCCAGCAGAG AGT/CJGGCCCC ACAACAAAAGAG GTCCAGC	T	C	Val	Ala (8024)	CONSER VATIVE	tm7 or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.3E-55	8
5854	cg43948839	798	TCCCAGCGCGT GGGCCGCGGCT CCA/CJGTCCG CCACCGCGCCT CCTTTGCCA	C	G	Val	Leu (8025)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. pcls:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17

5855	cg43948839	799	CCACGCGCGTG GGCCGCGGCTC CAC G C TCCGC CACC GCGCCTC CTTTGCCAC	G	C	Asp	Glu (8026)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17
5856	cg43936136	2321	TCTCCCAATTAT CTCGTTCACATC A A T A TAAAGTG ATGTCGGGCAGA CCAAAT	A	T	Phe	Tyr (8027)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa.	0	
5857	cg44130900	1488	AGAAACAATTTA GCACACTGGTCG A G T TCAACAGC AACTGCTGGAAA AAAAA	G	T	Glu	Asp (8028)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
5858	cg43920700	1055	GCCCCAAGTCCA TCGATGACAGTG A G T ATGGAGA GCCCTGTTGATG ACGTGT	G	T	Glu	Asp (8029)	CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NF1-X) (NF-1/X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.1E-243 (19p13.3 )	19
5859	cg43255478	667	CGGCTGCAGGC GGCGCACCACG GGG G TGGACG CGGGCATGGGT GACAGCCTC	G	T	Gly	Val (8030)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q92481 AP 2 BETA TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 449 aa.	5.4E-236	

5860	cg44012546	1960	ATCCGGAGGGC CGGTGGTCCGG GCG[C]/TGGGGA TCCTCTCCAGC GGTTCCTC	C	T	Arg	His (8031)	CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - MUS MUSCULUS (MOUSE), 551 aa.   pcis:SPTREMBL- ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF (ERF) - MUS MUSCULUS (MOUSE), 551 aa.	8E-199	19
5861	cg43947199	2208	CTTGGTGCCCGA GGAAAGGATGAA A[C/G]ATAAGTAT CTCGAGCATTTG TCTCA	C	G	Val	Leu (8032)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.   pcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.2E-158	8
5862	cg43982109	1818	CTCTGCTCCAGA CCTTCCCAGGGC A[C/G]TCAGCAC GCCCCACATGCT TCGGAG	C	G	Ser	Thr (8033)	CONSER VATIVE	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.6E-131	10 (7p)
5863	cg43918185	141	AGAGCCCGGCC CGACGCCGCCA TGA[G/C]CGCCG CGCTCTCAGCC TGGACGGC	G	C	Ser	Thr (8034)	CONSER VATIVE	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q03484 CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (TRANSCRIPTION FACTOR CELF) - RATTUS NORVEGICUS (RAT), 268 aa.	2.1E-122	8
5864	cg43918209	1269	GTTGGGAAAGG CGCCCTCCGCTT GC[G/C]CCGGAG GGGGCTGCAGG CGATCGGC	G	C	Ala	Gly (8035)	CONSER VATIVE	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.7E-115	19



5865	cg44910798	258	TGATGCCTAGTG AGACTTTGGCCT G/C/TJGGAAATC TCTATCACATATA ATTA	C	T	Arg	His (8036)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.7E-89	
5866	cg42849540	1841	TCCAGAAAGAGC TCTGCAGGCGG AGC/GJAAAGGC AGGGCAGCCGG AAAGCAGA	C	G	Ala	Gly (8037)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	2E-88	20 (20q13)
5867	cg42532030	318	TATAAATGTGAT GAGTGTGGGAAA G/C/GJCTTCAGTC AGAGCTCAGATC TTATT	C	G	Ala	Gly (8038)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.9E-57	
5868	cg43984952	620	CTGCTGCAGGAC AGCGACTGCAAG G/C/TJGTCTCCG GAGGGCCCGCA GGCCAC	C	T	Ala	Val (8039)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
5869	cg43984952	662	GAGGCCCAACAA CACGGCCTGGC CGC/TJCTCAGA AGCACGAGCCG CAACGAA	C	T	Ala	Val (8040)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)

5870	cg43984952	733	CTCGTCCCTTCAC CAATTAATCCCT GIC/GJAGAACC ACCAGACGCCTT CAAGGC	C	G	Gln	Glu (8041)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
5871	cg43998978	4041	GCGCCCTGGCA AATCCAGGAGAC AGIC/GJTCCGCC CAGCAGCTGGC CCCAGGTG	C	G	Ala	Gly (8042)	CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
5872	cg43976701	2368	CTCCCTTCAAAA GTCAACCCCTTCA C[G/A]CGTTCATA ATAATATGTATG CCTGG	G	A	Arg	His (8043)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0	
5873	cg43976701	2370	CCITTCAAAAGT CAACCCCTTCACG C[G/A]TTCATAAT AATATGTATGCC TGGGG	G	A	Val	Ile (8044)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0	
5874	cg44008864	1022	GGGATGATGGTC AGCTGAGAGCG CA[G/C]GTCATG GAGGCCGATGT CTGCCACA	G	C	Leu	Val (8045)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.   pcls: SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	

5875	cg44008864	3466	CACGTAGACCCA GAGGGTGATCA GGG[C]TCAACA GGAAGGGGCTG CACATCCA	G	C	Thr	Ser (8046)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.pcls:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
5876	cg43300953	418	CTGAGCAGCGC CTGGCGCAACAA CA[G/C]TGTCCC GCTGCGGGCTGC GGGACGGC	G	C	Ser	Thr (8047)	CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
5877	cg42876412	487	AGCATCGTGATG ACCACCTGCTCC A[G/C]CTTCTGTG CCTTGGGCATGA TGCCT	G	C	Ser	Thr (8048)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14
5878	cg42876412	532	ATGCCCTCTCCTC CTATACATCTAC A[G/C]CAAAGGG ATCTACGACGGA GACCTG	G	C	Ser	Thr (8049)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14

5879	cg43945806	591	GTAGGCCCAAT CCTTCACAGGG A/C/TGGAAATGAT GCTGCCAGTTCA CTGTC	C	T	Val	Ile (8050)	CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
5880	cg43269525	4020	TCTCTTGACACC CATAATTCTCCG G/A/TJAAGAGTCT TCAAGAACAGTT GCTCG	A	T	Phe	Tyr (8051)	CONSER VATIVE	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN--PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.5E-163	15
5881	cg43120117	2272	TTC AAGGCTTTG CAAGGTTCTACA G/G/CJCGGGGCA GGGCCCCGGCT GTTCAACC	G	C	Gly	Ala (8052)	CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN-- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
5882	cg43120117	2275	AAGGCTTGCAA GGTCTACAGGC G/G/CJGGCAGGG CCCCGGCTGTTC ACCATC	G	C	Gly	Ala (8053)	CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN-- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
5883	cg43944666	606	TGTAATGAAGA AGGTATTGAGAA A/G/CJAAAAAGA GACAACCAGGA GCATCC	G	C	Val	Leu (8054)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0	1
5884	cg43926985	1454	ACATGGATCCTC ATCCAGTTTGCA TT/GJTAGGAGGA CTGACAAATGGT AGTGG	T	G	Leu	Val (8055)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
5885	cg43978862	901	GCACATACTCAT CCTCATAGCCTT C/T/GJTCATCAGT CTCCCCAGTGGT GGGAT	T	G	Glu	Asp (8056)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa.	0	3

5886	cg43935402	1689	AACTCTACAAAG TGCCCCCCAGCA G/C/GJAGACCTC CTCGTCTCCACC TCCACC	C	G	Gln (8057)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
5887	cg43964609	877	CTGGGCATCCCC TTCAGGATCCAG G/A/CJCCACGGT CTGGTAAGCCCT GAAGTC	A	C	Val (8058)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa.	0	5
5888	cg43971826	1014	GATCTTACATCG AAAATGCCCTACA T/C/JTTTCAGTAG CTATGATATCAA ATGTA	C	T	Asn (8059)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13576 RASGAP-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 1575 aa.	0	5
5889	cg43924112	4797	ACTGGTTTAAAG GATTGAAGAATT C/A/CJCGCGTGA AGGGGAAAGTGT TCCAAA	A	C	Gly (8060)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
5890	cg43968933	1077	TACTGTCTCAT CTTGCTAGAATG A/G/AJAATTCCTG AGACCCCTTGAAG AAGAT	G	A	Lys (8061)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa.	0	6
5891	cg43999667	3945	GTTTGTGTCAGGA CTTTTTTTTCTA C/JAAGTTGTTTT TCTGGGATCACT GCT	C	T	Ile (8062)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
5892	cg43986140	4121	TTGTCCTTTGGAA CTTGATATTAAGT [C/J]GACACTGCC TACAGATCCCCC CTGT	C	T	Asn (8063)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14156 HYPOTHETICAL PROTEIN KIAA0143 - Homo sapiens (Human), 885 aa (fragment).	0	8

5893	cg43287089	1871	ACTACGTTCTCA GAGTTGCTGAAT G[G/C]AATACACA ACAAAAGAGGG GACAGT	G	C	Gly	Ala (8064)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa.	0	11
5894	cg43329920	1862	GTGGTCATCCTC TGATGACATCCG G[A/G]TCCTCCCA GCCAGAGGCCG GGCCCT	A	G	Ile	Val (8065)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12
5895	cg43916884	732	TTTCTGCAGCTG CTGCTTTGTCTT T[G/C]CAGCCCC CTTGGCTTTCTT GGCTGG	G	C	Ala	Gly (8066)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
5896	cg43924701	403	AGTGGGTCCACA TAGGAGGCATCT A[T/G]TCTTTGT TACTGCTACTTT CATAA	T	G	Ile	Leu (8067)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
5897	cg43924701	404	GTGGGTCCACAT AGGAGGCATCTA TT[G/T]CTTTGTT ACTGCTACTTTC ATAAG	T	G	Glu	Asp (8068)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
5898	cg43929104	1023	GCGAGGCAGGG CCAGCAGCAGG CGG[G/C]AGGGG ACGGCAAAACAG AACAGAAA	G	C	Gly	Ala (8069)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
5899	cg43055918	1732	CCCCTATAGGTA ATCCCGAGGGG TT[G/C]TCATCAA TGAAGCTATTCA GATGTG	G	C	Asp	Glu (8070)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17

5900	cg43964911	2446	GAACAGGCACA GGATGTAGGG GTA[G/C]TCAGG AGTGGCGGCAG CTGGACCAG	G	C	Thr	Ser (8071)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
5901	cg43927434	239	GGAGTCTTCATA GCATCTTCTCCA A[C/G]AGGTGCG AGGTCTGGGG GCTCCGC	C	G	Val	Leu (8072)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0	19
5902	cg43074645	3991	CTGTGAGCGCTG CAGGAGAGAGA AG[G/C]AGCGAG AATTAGAACTGC AGCGTCA	G	C	Glu	Gln (8073)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43152 KIAA0402 - HOMO SAPIENS (HUMAN), 1735 aa (fragment).	0	21
5903	cg17663981	395	CAAAAACCCCTGC AGCTGCCCAAA G[G/T]GGATGTC AACTACGCGTTT CTCCAT	G	T	Gly	Val (8074)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)
5904	cg43968854	6808	CTTGAAAGAGCT CTCCAGACACC A[A/G]TATGCACT GACAAAGCCAC GACTCA	A	G	Ile	Val (8075)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
5905	cg43968854	9484	AATATCCCTGCG CTCCAGACGCCA A[A/G]ATAAGACT GAGGCAGAAC GCAAAAT	A	G	Asn	Asp (8076)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
5906	cg43968854	9644	AAACCCATACCT AGAGACAAAGTC A[G/C]TGAGAAC AAAGGTGCTTGA GGTCT	G	C	Ser	Thr (8077)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)

5907	cg44026807	1745	ATTCGGGGTGCT CCCATCTCCTGC CA/GJTGCCAG GTTGCACATGAG AAGGAA	A	G	His	Arg (8078)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa.	0	2 (2p23.3)
5908	cg43960198	1974	GAAGAACCACGC CAGGCAGGCGG GA/GCJTTCGAG GTCTTGGACATC AAAGCTG	G	C	Val	Leu (8079)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
5909	cg43973129	1182	ATAAAGGGTTAT CCAGGCGTCCA GG[G/C]CCCTGA GGACCTGGAGT GGGAGCGC	G	C	Gly	Ala (8080)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)
5910	cg44016815	1158	AAGTTATTCTTG AACACAGGAAC [G/A]TGAAAAGCT TCAACAAAAAGA ATTA	G	A	Arg	His (8081)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75330 INTRACELLULAR HYALURONIC ACID BINDING PROTEIN - HOMO SAPIENS (HUMAN), 724 aa.	0	5 (5q33.2)
5911	cg44923983	299	CGCGGCACAG CGACGAGAACG ACG[T/G]TGGGC AGCCTCACAAA GGAGAAAG	T	G	Val	Gly (8082)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 790 aa.	0	9 (9q22.3)
5912	cg43311566	932	CACGACCTGCTC ACCACCTATGCC GT[C/T]ACCCACC CACAGGTGTCCT ACTGC	T	C	Val	Ala (8083)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
5913	cg43277466	2078	TTCTCTCTCTTT TCCCTCTCTCGCT G/CJGAGCTCTTC CAGCTCCTTTTG TTTC	G	C	Gln	Glu (8084)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	XY



5914	cg43139712	1736	AAGACCAGGGAA AGGGGGGAGCA GG[G]TGACAAA GAGGGGCCGGG GCAAGCAC	G	T	Gly	Val (8085)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	0
5915	cg43934688	1989	ATGGCTAAGAGA AAAACCAATTAC A[C/G]AAATTGAA GAGTTTCTGAT GTAA	C	G	Gln	Glu (8086)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	0
5916	cg43972478	2072	ACTATGTTAGGC TGGCTTCTATC A[A/C]CGCGTGA AGGGATGGGCA AGATGCC	A	C	Leu	Val (8087)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43284 HZW10 - HOMO SAPIENS (HUMAN), 779 aa.	0	0
5917	cg44003843	4744	CCAGCTGCCCC CTGCCCTTTGT GG[C/T]CCGGGG CAGCTACAGCAG CATCGTC	C	T	Ala	Val (8088)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	0
5918	cg44015572	1259	GCATTTATGCTC CAATCTGCATCA A[G/T]CAATAATT CTTCAAATACCT TCATT	G	T	Leu	Ile (8089)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16526 PHOTOLYASE-LIKE 1 (PHOTOLYASE HOMOLOG) - HOMO SAPIENS (HUMAN), 586 aa (fragment).	0	0
5919	cg44024279	1902	CAAATAACAGAG GAACAACTTGAG G[C/G]TGTCATTG CAGATTTCTCAG GCCTG	C	G	Ala	Gly (8090)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	0
5920	cg43956210	1440	CCTGTAATCCTT TCTGCTCCTTGG T[A/T]CTTAGATT TGATTAGCTATG GACAA	A	T	Tyr	Phe (8091)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)

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5921	cg43949262	1762	GTCCGTGGTGA GTCGTCCATGCA G[G/C]CCGGCAG CGCACAGTAAAT CTGGGA	G	C	Ala	Gly (8092)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
5922	cg43995003	988	GCTGTAGAGAAA GTGAAGCGCACA A[A/G]AGATGAG CTAGAAGTCATT CATCTA	A	G	Lys	Arg (8093)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
5923	cg40918088	1908	AAAAGCCACAGA GGGCCGGATCA TT[A/T]CAGTGA GGATCACTACCC GCAAGG	A	T	Thr	Ser (8094)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287 X (Xq28)	
5924	cg43931056	1283	GAGAGACATGGA CTTGATCATCAA G[T/C]AATTCTG TAACCTTCGAGA AAGCT	T	C	Val	Ala (8095)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
5925	cg43949830	1073	AGAGTCAGTCGG TTTGGACAGCAC A[C/G]TTTTCTG GATTCACCATTC AGACA	C	G	Ser	Thr (8096)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92817 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	18
5926	cg43930921	535	TGGGAGTGAAGT GCAGACACTTGG A[G/T]TCGATCCG CAGGAGCCGCTT GAGCA	G	T	Asp	Glu (8097)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92983 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
5927	cg43980328	717	TTGGTTGCTTA GCCTGGATACCA G[A/T]GGAGAAG ATGTCATCCATA TCATCA	A	T	Ser	Thr (8098)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

5928	cg43254830	1270	TTTAACATTCCAAAG AGCTCTGACCCA [G/C]AACAGATG CGACAGAGTTTG CTGAC	C	Glu	Gln (8099)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
5929	cg43962278	331	TTATGGCTTAGA C GAAGGGAACAG CT[C/G]AAAGAAG CCCTTGAAGAGG GTGAGG	G	Glu	Gln (8100)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa.	1.5E-250	2
5930	cg43973393	858	AAGGAATGTGCC A ATATATACAAAC A[A/G]AGCTCTCT GTTACTTGAAGC TGIGC	G	Lys	Arg (8101)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q07617 INFERTILITY-RELATED SPERM PROTEIN - HOMO SAPIENS (HUMAN), 528 aa (fragment).	1.5E-241	
5931	cg43928134	1540	TTCAGATGGAGA C GTACTTCTGAAT T[C/T]TACTATCA GAAATCCACAA AGATT	T	Arg	Lys (8102)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
5932	cg44013460	1020	CACTGAGTTGAA C AAAGCTGGACTT C[C/G]CAGCTCC AATTGGACCCAG CAGCAG	G	Gly	Ala (8103)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
5933	cg43962127	788	CGGCAAAAATCC C AACGTTGGGTGG A[C/T]AGAGGCG TCGATCATAAAG CACACA	T	Val	Ile (8104)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
5934	cg43916785	3427	CATTTCTCTTCTT C CTTTCTTCTTCTT C/T]TTTCAGCTTC TTTCTCATATTCC CG	T	Arg	Lys (8105)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14

5935	cg43994204	1312	GAGGCTCTGCTG CAGCTGTGCGAG GIC/TTCCTAAGCC TGATGGAACCTG TCAAG	C	T	Ala	Val (8106)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60864 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
5936	cg43994204	654	CTCCACCAAGGA GAGCTACCCGCA C[G/A]TCAAGACT GTCTGGGACGCA GCAGA	G	A	Val	Ile (8107)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60864 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
5937	cg43989168	308	CACCTCATTAC TCGTTTAGCTTT G[G/C]CTTCAATC CTCTGGCCACTT CCAAT	G	C	Ala	Gly (8108)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P70541 TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP- GTP EXCHANGE FACTOR) - Rattus norvegicus (Rat), 452 aa.	2.2E-215	1
5938	cg43062448	1357	TTAAAGGAATCC ATAAAATGGTGA A[G/C]TCCCAGG AGCTCCACAAAT GTAGCC	G	C	Leu	Val (8109)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3
5939	cg43049457	176	CTGAGCCGACAT CTTCACTCATCA AT/C]GTCAATTCT TGCTCTCTCTCC CCTCC	T	C	Ile	Val (8110)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	5.5E-212	2
5940	cg44021565	1285	ACGCTGACCCAT GGAGGCTGCAA AGT/A]GATCACT GCCTTTGTGGTG TCCACT	T	A	Thr	Ser (8111)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
5941	cg44021565	388	CCAGAATCCAAA GAGATTCTTAAA TTC/TCCACTTTT TCTTTCTTTTCAG TTCT	C	T	Asp	Asn (8112)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1

5942	cg44128902	964	AAGATGGAGTCA GCAGATCAGGC CGT/CJTGCTGA GCTCAACGGGA CCCAGGTG	T	C	Val	Ala (8113)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
5943	cg43967823	1057	GAGGACATGCTG GCTATGCCCAAG GIC/TJGGCGCTG CTCAACGACTGC GTGTGC	C	T	Ala	Val (8114)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
5944	cg43944615	1568	AGCTCACACTCT TTTCGGGTTTGT TIC/TJCTTCTGG GCACTCCTAGTT TTAAT	C	T	Arg	Lys (8115)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.3E-192	
5945	cg43973314	1045	GCAATTGCAAG CTTCCCCCAAT GIC/TJCTTGAGAA TTTCAAAAGAGG TAATC	C	T	Ala	Val (8116)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
5946	cg43968431	492	ATTCACCAACCCA CTTGGGTAAGGA GIC/GJCTTTGGG GTCCACCTGGG CCAGGTA	C	G	Gly	Ala (8117)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
5947	cg42374050	580	GGCTGGGTCAG AACCTGTTTAAT GGT/CJGGCCAG CTTCTTGACCC TCTTGGT	T	C	His	Arg (8118)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15335 CHONDROADHERIN - HOMO SAPIENS (HUMAN), 359 aa.	4.1E-191	
5948	cg43119894	1986	ACGGTCAGGGT CCACATAATGCA TTTC/TJTTTCAT GTCACATTCTTC AGCAGT	C	T	Arg	Lys (8119)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA75235 LACTOSYLCEAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa.	2.3E-190	2

5949	cg43926852	1689	AGTTCGGGAGG CCATCTGGATGG CTC/TJTGATCCA CTCTGTGCGCTC CTTGGG	C	T	Arg	Lys (8120)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
5950	cg43996402	1313	TGCAAAACCCACT GTTTCTCATCTC C/G/CJCTATTAGC TCCGAGGGGTG CATCGA	G	C	Ala	Gly (8121)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5951	cg43996402	653	TGCTTGTAACT ACCAGGACTTCT G/C/GJTCGGCT TCTCCGGCTCCT TTCCTC	C	G	Ser	Thr (8122)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5952	cg43996402	854	CTGGGCTTTTC CCGGTTATGGTG A/C/GJTGCTAGAA AGTTCTTCATGA AGCTT	C	G	Ser	Thr (8123)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5953	cg43249389	1134	AGAAAGTGGATCC ATTGCTTCGAGG A/C/AJGTCACGG CCATCATTTTCT GTGTCG	C	A	Asp	Glu (8124)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.4E-188	15
5954	cg43965001	785	AATGTGTCGCAG TTGGCTATTGGG A/AJGJCGTCCTTC ACAAAAATCCAG CTGAC	A	G	Val	Ala (8125)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD42861 NY-REN-2 ANTIGEN - HOMO SAPIENS (HUMAN), 570 aa.	1E-178	14
5955	cg43919917	1069	TGACTCAGAGCA GGTGCCCCCAGG CA/C/AJTCGGCC GGCTCCGCCCG CGCACCCCG	C	A	Leu	Ile (8126)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa.	3.5E-178	22

5956	cg43989723	422	CGGAGCTGCG GGCCGGAGCG AGGIC/TJTGAGAT CCGGGTCTTCCT CCAGCAG	C	T	Ala	Val (8127)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
5957	cg43989723	595	GATAACAGGGCC ACTGGAAGAAGC CIG/CJTGGCAGT GGCTTCTCGCA GGTGCT	G	C	Val	Leu (8128)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
5958	cg43926685	490	GTTCACTACAAT TCTAAATACAAG AIG/CJCTATGATA TAGCCCAAGATG CGCCG	G	C	Ser	Thr (8129)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	
5959	cg43329903	854	GTGGTCATCCTC TGATGACATCCG GIA/GJTCCTCCCA GCCCAGAGCCG AGCCCT	A	G	Ile	Val (8130)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.9E-167	12
5960	cg43315424	213	ATCATCAGGGAT GCTGGAGTCTG GCIC/GJCCCCC CACACCACGAGA GCTGAAG	C	G	Gly	Ala (8131)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
5961	cg43990820	411	GGCCCCAGGCT TTCTTCTTG CAIG/CJAACACTC TGCAAGGAGGC ATGCAGT	G	C	Leu	Val (8132)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.3E-150	3
5962	cg42929454	414	AAAGTCAGTGGT GTTCTTTTGAA CIG/CJCCAAGGC TAGAACACATTT TAAGCC	G	C	Ala	Gly (8133)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa.	1.1E-144	10



5963	cg42706411	220	CATCAGGTGGAGC GAGATTAGAAAC A/C/G/TATTGATA AAATAACTCAAT ATGTT	G	Thr	Ser (8134)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P32856 EPIIMORPHIN (SYNTAXIN 2) - Homo sapiens (Human), 288 aa.	3.8E-140	7
5964	cg43260991	315	GCGCCACACAGG GAGCCAGGAGC CTGT/GIGCGCA GGCCCATGCGC AAGTCCTTC	G	Val	Gly (8135)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
5965	cg43303845	863	AGAACAGCAACG GCAAAAGGAGCT G/C/GJAGCGGA AAGGCTGGAGC GAGAAAG	G	Gln	Glu (8136)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.9E-138	
5966	cg43962219	1066	TGCCACTCGCCA GTTTGCCAAAGA G/C/AJTCTACCAG ATTTTTTGAG GCATA	A	Glu	Asp (8137)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
5967	cg43984220	226	GGTCAGCGGG CACCAGGTGCT CT[G/C]GAAGAG CTTGAGGATGTG GTTCTCG	C	Gln	Glu (8138)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
5968	cg43950180	577	TATGGAATCACA GTTATCTCCTTG C/C/TJTGATTCA ATTTGGTTGAG AAGTG	T	Arg	Lys (8139)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q09996 PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS) - Caenorhabditis elegans, 1198 aa.	3E-131	5
5969	cg43918152	369	AACAGACAGTTA CGCAGCCATTTC A/G/CJAAGTGGAT CGATTGCAGTCA GAGCC	C	Glu	Gln (8140)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5E-131	9 (12q23)

5970	cg43928955	175	GCCTAGTACTCT TATGTGAAGTCT A/C/GJCAAGCTTG TGCTCAAGGGAA CCAAG	C	G	Thr	Ser (8141)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
5971	cg43917824	646	CCAGTGCCCAAC ATGACACCTTCA G/G/CJAGTCGGC CGGAGAGGCA CTCGTGT	G	C	Gly	Ala (8142)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.3E-128	16
5972	cg43931286	511	GTGTTTGAAGAC CCAGTCATCAGT A/A/GJATTCACCA ACATGATGATGA TAGGA	A	G	Lys	Arg (8143)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD2775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa.	1.4E-128	17
5973	cg43307940	438	TACATCCCCCTGG AGATGGCCCCACC T/T/CJCTTTTGG TCAGTTGGCAAA CCAGC	T	C	Lys	Arg (8144)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
5974	cg43067745	160	CACAGAAAGAGA TCACAGACTCCC T/A/GJCCCTTAGAA GAAGGGAGGTG GTAGAT	A	G	Val	Ala (8145)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
5975	cg43926002	390	CGGGCACAGAA ACACAGCAGCG GGA/G/CJGAGCA ACACCAGCACTG CCAACAGA	G	C	Ser	Thr (8146)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
5976	cg41045063	611	AGCTTCCACCAA GGTTGTACCAT G/C/TJCTCCAG CGCCTGACGCC CCTGGCC	C	T	Ala	Val (8147)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa.	3.3E-102	19 (19p13)

5977	cg43980312	2657	AACAGTATCTTT GGAAGTGGTCG AG(A/T)GTGTGTC AGCTCTGGACTC TCTACA	A	T	Ser	Thr (8148)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5978	cg43252708	534	CCTTGCCGAGAG ATTGACGTGTC C[G/A]TTTGCATC CTGGGCTCCCT CGCTT	G	A	Val	Ile (8149)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5979	cg43927693	713	GTATGGCGGGA CAACCATGGCTG GC[G/A]TGGGG ACGGCGGCTGC CAGAGTGA	G	A	Arg	His (8150)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
5980	cg42835634	532	TACTGTGACTTC TTCTACTTGAT G[G/T]GACCAAA GGTAGGTCCTG GGATGAC	G	T	Gly	Val (8151)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa.	3E-92	22
5981	cg43921592	453	CCCCGGATGTG GATACCTATAAG GA[G/T]ATTTCAT ATTTGTTGCGG AGTTCA	G	T	Glu	Asp (8152)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
5982	cg43978148	536	GGAGAATTGCCA GACTTGTTGTAC C[A/G]ATTATATC ATCTCAGTCTTG AATT	A	G	Asn	Asp (8153)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16

5983	cg43978148	690	GAAAAAGAGGTT GTTGCTGTAGCC C[A/G]TGCTGTTT ATCAAGCAATGC TCAGC	A	G	His	Arg (8154)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16
5984	cg43059113	456	GCACTCAGCAGT GCGTGCTTTTTC TTTCTGGGAAA GGCAGGACAAAC CAGCTT	T	C	Lys	Arg (8155)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
5985	cg43960450	1409	CTTTTCCTGCAG ACGTTCAATAAT A[G/C]CAGCTAG ATTAGCCTCAG GTTTTT	G	C	Ala	Gly (8156)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5986	cg43960450	1544	TTCTCGCTCGTG TTCCCTCTTCTC T[G/A]CCAAATTGT TTCAGCACCTGG GCCTC	G	A	Ala	Val (8157)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5987	cg43955651	519	GCCACACTCTCT GTGCATCGGCTT G[C/T]GCGTGTC CGGGTGGAGG AGTTGAA	C	T	Arg	His (8158)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5988	cg43922714	227	GAACTAGAGAGAA ACATTAAATTTA [A/G]AGAAGCTGT TGTTTTAGGGAG CACG	A	G	Lys	Arg (8159)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa.	9.8E-87	19
5989	cg43996941	481	TGAAGAAACTC AGCTAAATTTCC TT[G/A]TAGGAAG GAGAGATTTTGA CATGCT	G	A	Val	Ile (8160)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16044 PREPRO-MELANIN- CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa.	3.1E-83	12 (12q23)

5990	cg43920730	849	TTTTCTCTTTG TTTGTCCACTA C/GAAGCTCACT TCTCAGAGCTAA ACTC	C	G	Val	Leu (8161)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15182 CENTRIN - HOMO SAPIENS (HUMAN), 167 aa.	5E-83	
5991	cg43969140	528	TCGGCCCCACTC GCCAGTCACAA G/GA/CATCATTA ACACTCAGACAG GCCAC	G	A	Ala	Val (8162)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5992	cg43969140	595	GCCTTCAGAGCC TCAGCCTGCTCC A/C/A/AAACCCCTG GCAGGTGTGTCT TGGAA	C	A	Val	Leu (8163)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5993	cg44936941	716	AAAATACCAAC AGTTATTGCGTA C/C/TJTTGTAGCA TATGCTGGTTGT ACTTC	C	T	Arg	Lys (8164)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
5994	cg44936941	755	TGGTTGTACTTC ATGAGGGTTGCG A/C/TJGGTCAGAC CAGAAAAACAGC AGTCT	C	T	Arg	His (8165)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
5995	cg38622616	345	AGAATTCTTCAA TTTCACCTTCATC [G/C]TCCATGG TTCTTCTAAACTT GGAC	G	C	Asp	Glu (8166)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40849 SIRTUIN TYPE 1 - HOMO SAPIENS (HUMAN), 555 aa.	6.3E-76	
5996	cg43969639	959	CCAGACCCCACTC TGCAGTAAGGTG TTT/ATCAAAACA GAAAATGCACAA ATGAA	T	A	Glu	Asp (8167)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3

5997	cg42696021	427	GCATGCTTCACA CAGTGGCTGTGC C/GA/JCCTTCACA ATGAAGTGAACC GGAAG	G	A	Arg	His (8168)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
5998	cg42696021	481	GGCAAGCCTGAT TTTGACTGCTCA A/GA/JAGTTGATG AGCGATGGCGT GACGGC	G	A	Arg	Lys (8169)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
5999	cg43942922	344	GTACACCTCTGAG CCCACATCTCAG G/C/TJCACTAGG GGAAGAAAAAT AGGTCC	C	T	Ala	Val (8170)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6000	cg43955219	1361	GCCTCATGCTCT CTGGGATTGCAG A/C/GJCATCCAG GTCTGTCTTCGC CCCTGT	C	G	Asp	Glu (8171)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
6001	cg43927424	302	AGCGCAGTATT CAGAGAAAAAGTA T/TJCTCTTCAG CTGAAGTACCCG CACCT	A	T	Thr	Ser (8172)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6002	cg43927424	366	GTCGGGCAGGA ACAGAAACACAC CTA/TJCTGCCA CTAGAAGTCTGT AATAAT	A	T	Tyr	Phe (8173)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6003	cg43082068	765	TTCTCTGGAGCTG CTGGTGAAAGAA A/C/GJCTCTGGA GGCCCGGACTC CCCGGAC	C	G	Thr	Ser (8174)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:G2352941 LEUKOCYTE- ASSOCIATED IG-LIKE RECEPTOR-1 - HOMO SAPIENS (HUMAN), 287 aa.	2.5E-65	

6004	cg42381630	271	TTGGCCTAGACC AAGGCGCTATGT A[C/G]AGCCTCCT GAAATGATTGGG CCTAT	C	G	Gln	Glu (8175)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
6005	cg43950549	466	TGACTGGATTAA AAGGTGTCAAGA A[C/G]TTCAGAA GGGTCAGAAATAG GAAGT	C	G	Leu (8176)	Val (8176)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6006	cg43308257	839	TCAGAGCCGGC GGTGGTGCAGA AGA[G/A]AGCCA GTGGCCAGTGA CCACACAGC	G	A	Arg (8177)	Lys (8177)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
6007	cg40968986	269	TGAGCTGGAGCA GGAGCAAGAGA GA[G/C]AGGGCT CCAGAAATCATTG CCAGAA	G	C	Glu (8178)	Gln (8178)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58 (11p15.2)	11
6008	cg43052776	401	ACCAACAAAGAT TTCAGGGATTTT G[T/C]CAGGGAG AAAAAGTATCGG ACAGAA	T	C	Val (8179)	Ala (8179)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment).	3.6E-57	
6009	cg43942680	697	CTCGGAGGAGA GCGCCCTCAATC AC[G/C]TGCAGC ACCCGAGCGAC GAAGCCGA	G	C	Val (8180)	Leu (8180)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa.	1.8E-55	10
6010	cg43511804	864	GGGCTGATCTT CATACTCATCTT CT[T/C]TCATTGAG TACCATGACCCC TTCCA	T	C	Lys (8181)	Arg (8181)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4

6011	cg44341803	864	GGGCCTGATCTT CATACTCATCTT CT/CJTCATTGAG TACCATGACCCC TTCCA	T	C	Lys	Arg (8182)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
6012	cg43291028	1907	CTCTAGGCCCTT GAGCTGATACTG A[G]ATGATGGTG GCATTCTTTATCT TCAC	G	A	Thr	Ile (8183)	NON- CONSER VATIVE	angiopo etin	Human Gene SWISSNEW-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1124 aa.lpd:SWISSPROT-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1124 aa	0	9
6013	cg43921977	2748	ATTATTCATCCAA T GTTTCATATTA T/CJCTTCAAAAAA TTCAGGGAGATC CTG	T	C	Asp	Gly (8184)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20
6014	cg43921977	2753	TCATCCAAGTTT A CCATATTATCTTC IACJAAAAAATTCA GGGAGATCCTGA AAGT	A	C	Phe	Leu (8185)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20
6015	cg43921977	2754	CATCCAAGTTTC A CATATTATCTTCA IACJAAAAAATTCA GGGAGATCCTGAA AGTT	A	C	Phe	Cys (8186)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20



6016	cg43948568	2080	CCAGAGCCTGC CCGCTGGATGTC CTA/CJGATCATA TGGGGCCTGAA CAGCTCG	A	C	End	Glu (8187)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa.	2E-222	1
6017	cg42913771	469	GCTTGTTCAAAG GAGACAAGTGTC A/GC/JAGCCTGG TTGGAACCCCA AGATAT	G	C	Gln	His (8188)	NON- CONSER VATIVE	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
6018	cg43277632	1703	GACTGCAACAGT TCTTTATAATCCC T/GJCTGTAATTA GCCCAGAAAGAAC TCAG	T	G	Ser	Ala (8189)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
6019	cg43277632	774	AGCATGAAGGTT TCCCTGGAACAA G/GA/JCAGTGCC ACTGTGAAATAT GTGCCA	G	A	Gly	Asp (8190)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
6020	cg43252813	1307	CCAGAATCCCTG AGAAAAGCAATA G/AT/JGGCTGTAT CACCGGGGCTAT ATAGA	A	T	Glu	Val (8191)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.   pcis:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)	

6021	cg43252813	3832	CTCAAAATGCTCT TAATGCTCAGCA GIC/TATAAAGTC CTCATTGGTAAC CGGGA	C	T	His	Tyr (8192)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.lpcis:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)
6022	cg43931944	268	ACTATTCAGGTG TATGAAGAACT TTC/GTGGTGTGT CTGTTGGAGATC CTGTA	C	G	Ser	Cys (8193)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0
6023	cg43939527	1246	AGATGACCTCTC TGGTGCTGACAT C/CAC/JAGGCAATC TGTACAGAAGCT GGTCT	A	C	Lys	Gln (8194)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P49014 26S PROTEINASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa.	14 1.5E-233
6024	cg43958825	197	GTGGGTGAGCT CCGTGGCACCC CTG/C/G/GCAGT GCGATCATGCC GCCTCCAC	C	G	Arg	Pro (8195)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	11 7.8E-228
6025	cg43958825	198	TGGGTGAGCTCC GTGGCACCCCT GC/G/C/CAGTGC GATCATGCCCGC CTCCACA	G	C	Arg	Gly (8196)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	11 7.8E-228
6026	cg43933600	304	GCTCCAGGAGG AGGGCCGAGAA GGT[G/T]TGACC TTGTCTGCCCCC CGCACCT	G	T	Asn	Lys (8197)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	19 4E-185

6027	cg44026571	415	GGAAGTTATGGG TTTGATGCTTGG A/A/G/AATTTGTT GATGATTATACC GTCAG	A	G	Lys	Glu (8198)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:O00487 26S PROTEASOME-ASSOCIATED PAD1 HOMOLOG - HOMO SAPIENS (HUMAN), 310 aa.	3.8E-164	
6028	cg43284434	1995	ACTAACTTATATC GCAGAGTGGA [G/A]GGGGCCTC CTGGAGCACAAG ATGGG	G	A	Gly	Arg (8199)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4E-121	6
6029	cg43251803	2910	GGACCATCTGAG TCCACGTACTGC C[G/A]GCGTTTGA GGTAGCAGGAC ACTGCC	G	A	Arg	Trp (8200)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
6030	cg43251803	2981	ATCTGAATCTGC TCGGTACGCACT C[G/A]TTTCATGA CTGAACATCCCA GGCGG	G	A	Arg	End (8201)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
6031	cg43132502	357	GCTGGCCCCAG TGCAGTGGGTG GCA[C/T]CGCCG AGGCTGCTGTTA CGGCTCAT	C	T	Pro	Ser (8202)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6032	cg44000476	1164	AACGGTCTCAGA GGCTGGGTAATC T/A/C]CCTGAACA GCTCCCCCATGG GCACC	A	C	End	Glu (8203)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:P78344 P97 - HOMO SAPIENS (HUMAN), 907 aa.	3.8E-53	3
6033	cg43966234	1864	TGGAAACATGAG CATTGAGTTCTT [T/G]GTACAGTGT ACAAAGGTGAATA TCCTT	T	G	Cys	Gly (8204)	NON- CONSER VATIVE	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0	13 (13q32)

6034	cg43255401	810	GCTGGAAGTGG AGCCCGTGGGA ATGACJCGCGT GAAGGGGACCG CGTGGAAT	A	C	Thr	Pro (8205)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P43121 CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA- ASSOCIATED ANTIGEN MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE) - HOMO SAPIENS (HUMAN), 646 aa.	0	11
6035	cg44026834	1466	CTGCCCGATGGA GAGCGTAGAAC GTTC/AJATCGCTG TACATAAGGAAG CTGTGG	C	A	Asp	Tyr (8206)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6036	cg42558238	2115	TGACTGGAATAA CCAAAGCCCTCCC CTTCJACACACAGC CAGAAAGCTGAGA TTGGA	T	C	Tyr	His (8207)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.  cds:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1 )
6037	cg43956560	1285	CTGGCAAGGAG ATTAAAAAAGG CAJATJGAAATCC AAGAGAAAGTATG AATGAC	A	T	Lys	Met (8208)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)

6038	cg43956560	1287	GGCAAGGAGATT AAAAAAGGCAA GATTAATCCAAG AGAGTATGAAT GACCC	A	T	Lys	End (8209)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)
6039	cg42388009	378	AAATGAAGGAGA AAACAATGAAGA AIC/TJCGAACGAA GACGAAGACTCT GAGGC	C	T	Pro	Ser (8210)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7E-172	4
6040	cg42388009	379	AATGAAGGAGAA AAACAATGAAGA CIC/TJGAACGAA GACGAAGACTCT GAGGCT	C	T	Pro	Leu (8211)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7E-172	4
6041	cg43303099	965	GAGACGGGAGG CCCGGGAGAAC TTG/C/AJCGGTCT TTAGCTTCCTAG GACCCAT	C	A	Pro	Thr (8212)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa.	8.7E-158 (19p13.3)	19
6042	cg42926989	269	GCTGGCAGCAC AAAGGCTTATCG CA/C/TJGAGGAA GATGCAGCCACT CCTGCT	C	T	Val	Met (8213)	NON- CONSER VATIVE	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136 (14q11.2)	14
6043	cg43980411	1284	TTCTTATTGCA TAAGATAACCAA C/GJTGCAATTTAT TTTTGGCAGAT TTT	C	G	Asn	Lys (8214)	NON- CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222 (18q21.3)	18

6044	cg43980411	1310	TGCAATTTATTTT TCGGCAGATTTT[ C/G]CTCACCTA AAACTAAGCGTG CTGC	C	G	Ser	Cys (8215)	NON- CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
6045	cg43971453	2657	TGTCCAGCCATG AACTGTCCAAAG C[G/C]AGGGGGG AAGGTCAGCGTG GAGATG	G	C	Arg	Gly (8216)	NON- CONSER VATIVE	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
6046	cg43970982	2131	TGGACCTCGGG GAAGCGGAGGT GCC[G/C]CTGGT GCTCCTGGAGAA CGAGGCAG	G	C	Ala	Pro (8217)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6047	cg43970982	2222	GGACCAAAAGGA GGAATCGGCAAC C[G/C]GGGCCCT CGTGGGGAGAC GGGAGAT	G	C	Arg	Pro (8218)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6048	cg43970982	4398	CAGCGCCAAACT CCACTGGGAGA GG[C/G]CTGAGC CCCCCGGTCCTT ATTTTA	C	G	Pro	Ala (8219)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6049	cg43131198	5672	GGCTCACAACG GTGAAAGCAGAC TT[G/C]GAGTTT CCTCTGCTCCAG CACCAG	G	C	Leu	Phe (8220)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa.	0	2 (2q36)
6050	cg43970983	2792	CTGCGCTGGGA GCCGGTGCCCA GAG[C/A]GCAGG GCTTCCTTCTGC ACTGGCAA	C	A	Ala	Glu (8221)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)

6051	cg43970983	9090	ACGTCCGTTATT TCAGTGACTTGG TTCATCCGTGGG TCTAGCCTTCCC CCCTGT	C	A	Pro	Thr (8222)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
6052	cg41035069	1211	AATGGAGAAAAT GGTTTGAAGGT GATCTTGGGTC CTCATGGTCCAC CTGGC	A	T	Asp	Val (8223)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6053	cg41035069	1438	AGGAATACACCA AACTCTGGTGG ATTGJATTATAAC AAGGATAACAAG GGAAA	T	G	Tyr	Ser (8224)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6054	cg41035069	1441	AATACACCAAAC TCTTGGTGGATA TTTGJATAACAAG GATAACAAGGGA AATGA	T	G	End	Ser (8225)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6055	cg43991318	3625	TGGATGCCAGG GTCTCCCTGGC TTCGJGTACAGG ATCACCCAGGCTC CCCTTT	G	C	Gly	Arg (8226)	NON- CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
6056	cg44032748	1860	ACCTCAGAATGG AGGGGCCTCGT GTCTTCAGGGC GGAAAGTACAGA CGCAGGC	C	T	Pro	Ser (8227)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 584 aa.	0	1 (1p32)
6057	cg43281450	1987	TCAGCCTGGCAG GAATGCCTGTCT TTCCTCTGAAGCT CATAGCCTGGAC GGCAG	C	T	Glu	Lys (8228)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)

6058	cg43281450	2082	CTGGGGCTGGG GATCCTCCTCCC CTG/AJATTGCT CGGGAAGCAC ATTATC	G	A	Ser	Leu (8229)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)
6059	cg43933757	1351	ATGGGCTCTTGA AGAGTATCTGGA TJA/GJAATTTGAC CCCTGTCATTGC CGGCC	A	G	Lys	Glu (8230)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
6060	cg43029279	607	TCTCAGGATCA ATTACATGTTG CJA/GJAAATGGAT GGTCAGCACAAAC CAATT	A	G	Gln	Arg (8231)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
6061	cg43029279	805	ACATGTAGTAAT GGAGAGTGGTC GGJACJACCACC TAGATGCATACA TCCAIGT	A	C	Glu	Ala (8232)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
6062	cg43956185	1009	TTACTCATCTGT CTCGACACTATA TJA/GJAGCATTTT GTACTGTGGGC GGATTG	A	G	Tyr	His (8233)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-180	1
6063	cg43956185	1266	TGGTGACCATCC TTCTTCTGTGCA T[G/JTTATGCGA GTCCAAAATGAT TTTGA	G	T	Thr	Lys (8234)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
6064	cg43956185	609	AAATTCAGCTGA TTCACCTGTTCT CJA/GJAATAAAGC TTCTGTTTGGCT GTCCA	A	G	Leu	Ser (8235)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1



6065	cg42542496	344	TTGCTCCTCGTG GTCAATGCTTCTC CT/CJAACGTGCA GGCTAACGCTGT CCAGC	T	C	Leu	Pro (8236)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-189	3 (3q26.3)
6066	cg42542496	650	TCATCCCTCCTG GGGCAGCTTTCT GIG/AJACAGGTC CGTCTCCTCCTT GGGGCC	G	A	Gly	Glu (8237)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-189	3 (3q26.3)
6067	cg2752665	551	CCGGAAACTTCC TGTGCAACCCAG AT/CJTATCACCT TTGAAAGTTTCA AAGAG	T	C	Ile	Thr (8238)	NON- CONSER VATIVE	csf	Human Gene Similar to SWISSPROT- ID:P04141 GRANULOCYTE- MACROPHAGE COLONY- STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa.	5E-75	5 (5q31.1)
6068	cg34413296	435	GCGCTACGGGG ACGTCCTGCAGA TC[C/A]GCATTGG CTCCACGCCCGT GCTGGT	C	A	Arg	Ser (8239)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYP1A2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.[pds:SWISSPROT-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa.	4.6E-278	15 (15q22)

6069	cg40333008	607	GCTGGTGCCACT CCTTCTCATTGT G[C/A]TGCAGCG CCACAGATTGA TGATAA	C	A	Gln	His (8240)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. pcis:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.9E-274	10 (10q24.3)
6070	cg43063374	1580	TGATTGCTTCCT GATCAAAATGGA A[C/A]JAGGAAAAG CAAAACCAACAG TCTGA	A	C	Lys	Gln (8241)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.	3.2E-254	10 (10q24.1)
6071	cg43063374	1591	TGATCAAAATGG AAAAAGGAAAAGC A[C/A]AACCAACA GTCTGAATTCAC TATTG	A	C	Gln	His (8242)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.	3.2E-254	10 (10q24.1)
6072	cg43966704	576	CCGCCAGGGAT CACAGCAAGGA GGT[T/A]GTCCCA GCCGCCCGTGA CACCCCCCA	T	A	Asn	Tyr (8243)	NON- CONSER VATIVE	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
6073	cg43966704	597	AGGTTGTCCAG CCGCCCGTGAC AC[C/A]CCCAGC ATGCTTCTCAAT CAGTTCT	C	A	Gly	Cys (8244)	NON- CONSER VATIVE	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11

6074	cg43962888	453	GACTGGGTTGGA GAGGAGATCAT GICATJGGCTGC AAAGAAGGGACT GGACCC	C	A	Leu	Met (8245)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
6075	cg43923204	1812	GGTGACCGACAT CATGCAGTAGCC GICJCCCGGA GTAGTCTTCACG GAGGCC	C	T	Gly	Asp (8246)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.7E-52	17
6076	cg43923204	1924	GGGCCAGCATC GAGGCTGCCCC TGGICJCGCTGT CCAGCCCATGAC AGGCCGG	C	T	Ala	Thr (8247)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.7E-52	17
6077	cg43967318	1615	TATTTTCTTCT GGGCCTTTGTGC ICIAAAGAGCA GGATGCCCTTGA AACCG	C	A	Gly	Cys (8248)	NON- CONSER VATIVE	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6078	cg34396112	1048	CACCCCATAGCT GAAGTAGTGGAA GIGCJGGTTCCC TGAGTTAGTCTC AAAGCT	G	C	Pro	Arg (8249)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6079	cg34396112	2946	TCTGAAGGACTG TCAGGTAGAACT TIGCJAAGAAGAA GCTGAGGGTGA GGGTGC	G	C	Phe	Leu (8250)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6080	cg34396112	2949	GAAGGACTGTCA GGTAGAACTTGA AIGCJAAGAAGCT GAGGGTGAGGG TGCACC	G	C	Phe	Leu (8251)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)

6081	cg34396112	2952	GGACTGTCAGGT AGAACTTGAAGA A[G/C]AAGCTGA GGGTGAGGGTG CACCGGA	G	C	Phe	Leu (8252)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6082	cg34396112	3012	TGCCACCAGGG GCATCGGGAGG CAG[A/C]TGCAG CTCCTCTGCCAG TCCTGCAC	A	C	His	Gln (8253)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6083	cg34396112	3498	CTTGCTTCCCAG CAAACCAAGCGCA G[C/G]TGCTCCA GGACCCCTCTGA ACACCT	C	G	Gln	His (8254)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6084	cg34396112	3721	CTCAATGCCAAT CTCCGTGTTCCTC C[A/T]CGACCCAG CTTGGCGTCAGG GTGCTG	A	T	Val	Glu (8255)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6085	cg34396112	3806	GCCTGTATCCAC GTCACACGCTCC C[C/T]TTCAAATC GCAGCTGCTTCC GAGGA	C	T	Gly	Arg (8256)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6086	cg34396112	3925	CTCTGGTTTGAA TAAAGATGGCGA G[A/T]GGCTGACT GAGTGGTCTTTC TTCTG	A	T	Leu	His (8257)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6087	cg34396112	3983	CAGCAATTTGGA TTATTCCCATCT C[C/T]TCCACAGC ATCCACCATCCC TGCCA	C	T	Gly	Arg (8258)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)

6088	cg44033747	1336	CTTGGCGAATAT GGCTGCCATGTT T[G/C]GAATCTAC CATGGTCCCAT GGGCT	G	C	Gly	Arg (8259)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0 9 (9p22)
6089	cg43314766	1220	TAGAATACCCCA TGGTGTCGCAAT TT[C]AACAGCAT TGTCGAAGTCGG CATCA	T	C	Lys	Glu (8260)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDHII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.2E-273 9 (9q21)
6090	cg43996714	1790	ACAGGCCGGGG ATAAGATGGTCC AG[C/A]TGTGGC CTGTAGGGGCG AAGGTGCT	C	A	Ala	Ser (8261)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2979825 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266 11
6091	cg43996714	2474	CCCTTCACCAGC CCTACGCTTCGG C[G/A]GCCAGGG AAGCCCCACAAGA TAAGGC	G	A	Arg	Cys (8262)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2979825 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266 11
6092	cg43330439	729	GCCTAGCAGCTG TCCAAAGTACAC CT[C]GGTGGTC AGCAGGATGCA GGCCCCAG	T	C	Gln	Arg (8263)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257
6093	cg43057018	1639	CTTTGAAGATG CCAGGAGCAATT C[G/A]GAATACTA TCTGATTGAATG TGAAC	G	A	Gly	Arg (8264)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.lpcis:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209 4 (4q22)

6094	cg44986087	939	CGCCAGCTTGAA GGCATACTCGGC A/TATGCGCAG GGACTTGGCCTT GGTGAT	T	A	Asn	Ile (8265)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P51553 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT GAMMA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 393 aa.	9.6E-207	X
6095	cg44917703	1242	GGCTACAGCACC ACAAACCGACTTC A/T/C/CAAGTCTG TCATCGGTCACC TGCAG	T	C	Ile (8266)	Thr (8266)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6096	cg44917703	1247	CAGCACCACAAC CGACTTCATCAA G/T/G/CTGTCTC GGTCACCTGCAG ACTAA	T	G	Ser	Ala (8267)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6097	cg44917703	1266	ATCAAGTCTGTC ATCGGTACCTG C/A/C/GACTAAAG GGAGCTAGAGC CCTTTA	A	C	Gln	Pro (8268)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6098	cg43923979	864	AAAATCTTTTGA CTGAGCTTCCGG A/G/A/GAAATTCA AAAGGAACCCCA TACAT	G	A	Pro	Leu (8269)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192 3 (3p13)	
6099	cg43960596	296	CCTGGGCTGTAG CGGGTTCGGGG GT/G/TTCGAGCA GTCAGGGCATG CTCCAGG	G	T	His	Asn (8270)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. <i>ipds</i> :SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.4E-170	12

6100	cg43960596	857	TCCACCCACTTG GCTGCCTGCTG GA[A/C]GCTCTG GGGATCAGTGAT ATCCAAC	A	C	Phe	Val (8271)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. pcls:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.4E-170	12
6101	cg43969759	919	AGAAATCTGCTCC GTGAAGGCTCCT G[C/T]GATGGCA GCAACACCTATG ATGGCT	C	T	Ala	Thr (8272)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6102	cg43969759	1199	CAAAACACGTGAT TGGAAGGCTTGT T[G/C]TTGGTGAT TCGCAGAGCAG CCAAGA	G	C	Asn	Lys (8273)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6103	cg43969759	431	GTGTAAGGAGT CATAGTCTGGAG T[G/T]TAGACCAG GGATCTTACAAA AGCCT	G	T	Tyr	End (8274)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11

6104	cg43248620	1748	AGGCCCCCTTCC TGCCGCCCGG GGATTCGGGA CCCCCGTTGAA GACCACT	A	T	Ile	Asn (8275)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0	1
6105	cg40993080	3300	TGGGCGTGCCC CTCTCTCTCCC CTT/GJGACGGT TTTCTCTGCCAT TTCTTG	T	G	Lys	Gln (8276)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6106	cg40993080	3302	GGCGTGCCCCCT CTCTCTCTCCCCT TCJA/TJCGCGTTT TTCTGCCATT CTTGTA	A	T	Val	Glu (8277)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6107	cg40993080	3306	TGCCCCCTCTCTC CTCCCCCTTCACG C[G/T]TTTTCTCCT GCCATTCTTGT ACTCA	G	T	Arg	Ser (8278)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6108	cg40993080	3307	GCCCCCTCTCTCC TCCCCCTTCACGC G[T/G]TTTTCTCTG CCATTCTTGT CTCAT	T	G	Lys	Asn (8279)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6109	cg42913756	366	GGCAGCCAGCT CCAATCCCAAAG GG[G/T]CCCAGA TGCAGCCGATCT CCCTCCC	G	T	Ala	Ser (8280)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P48378 DNA BINDING PROTEIN RFX2 - HOMO SAPIENS (HUMAN), 723 aa.	0	19 (19p13.3 )



6110	cg43988954	670	CCGGTTTCGAAG ACCATCCAGGCG GG/AJAGCCAC ACCAATGGAGAA GTGGTC	A	Ser	Phe (8281)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSNEW-ID:Q15633 TAR RNA BINDING PROTEIN (TRANS- ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa.   pcis:SWISSPROT- ID:Q15633 TAR RNA BINDING PROTEIN (TRANS-ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa.   pcis:SPTREMBL-ID:Q12878 TAR RNA BINDING PROTEIN 2 - HOMO SAPIENS (HUMAN), 366 aa.	6.4E-194	12
6111	cg43955901	755	CTGCAAAAGCATT GTGAGCTGCATC A/C/TJTTGTGCA TTGCCACAGGAG ATACC	T	Ser	Asn (8282)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.   pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.   pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.4E-97	2
6112	cg43955901	770	AGCTGCATCACT TTGTGCATTGCC A/C/AJAGGAGATA CCGGAGCCCATG ACAGAC	A	Cys	Phe (8283)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.   pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.   pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.4E-97	2

6113	cg43130017	338	TGAAGCGATGCG AGATACCTGAAG GTTC/TTTCCAC ACTGCTTGCATT CATAC	T	C	Thr	Ala (8284)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.9E-95	
6114	cg43918693	4135	AGCTTCTTGTCG TTCATCAGCTGC AIGT/CAGGTAAT CTGGGGTGGGC TTCGGC	G	T	Leu	Met (8285)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.6E-74	6
6115	cg43327954	1115	CAAGTGGAGGAT GATGGGGATGG CGA/GJTTACATG TCTGAGCCTGAG GCTGTG	A	G	Asp	Gly (8286)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6116	cg43327954	1434	GCATGAACCGCT CGGAACAGGTCT TTC/AJACGTGCTC TGTGTGCCAGGA GACAT	C	A	Phe	Leu (8287)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6117	cg43327954	1435	CATGAACCGCTC GGAACAGGTCTT CJA/CJCGTGCTCT GTGTGCCAGGA GACATT	A	C	Thr	Pro (8288)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6118	cg43946971	1232	TCACCGAGTACT CGAGCTTGTTATA A[G/C]GACCCAG TGGTGCACACAC ACTGCA	G	C	Lys	Asn (8289)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.9E-52	6 (6p21.3)
6119	cg43269465	324	AGGAGCTGGTC GAACCCAGCTGC GGT[C/A]CTCCTC ATTCACCAGTCG GTCCCGG	C	A	Asp	Tyr (8290)	NON- CONSER VATIVE	dynein	Human Gene Homologous to SPTREMBL-ID:Q27810 DYNEIN HEAVY CHAIN ISOTYPE 6 (EC 3.6.1.3) (ADENOSINETRIPHOSPHATASE) (ADENYLPHOSPHATASE) (ATP MONOPHOSPHATASE) (TRIPHOSPHATASE) (ATPASE) - TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN), 1125 aa (fragment).	9.7E-111	

6120	cg43950268	2402	TAGAACTCCTCA TGTTGCCACTCA C[G/C]GACATCCT TGGGTCCATCA TCCAG	G	C	Arg	Gly (8291)	NON- CONSER VATIVE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6121	cg43982507	2645	GCCAAATAATTC ACTGGATCAGAG CTT/AJAGCCACTC TAGTCAACAACC TGAAT	T	A	Leu	Gln (8292)	NON- CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
6122	cg43945212	1793	GTTGCGCGCGG AGCCCTATCCCA CGT/CJCGCGCT TCGGCAGCCAAT GCATGCA	T	C	Ser	Pro (8293)	NON- CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.8E-232	7
6123	cg41554010	1092	GGTGACGACGAT GGAACAGCTCAG G[C/A]JAGAACTG GGCCCCCATGC GGGGGA	C	A	Gln	Lys (8294)	NON- CONSER VATIVE	eph	Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.   pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.8E-203	11 (11q23)
6124	cg41554010	1093	GTGCAGCAGATG GAACAGCTCAGG C[A/C]GAAACTG GGCCCCCATGC GGGGGAC	A	C	Gln	Pro (8295)	NON- CONSER VATIVE	eph	Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.   pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.8E-203	11 (11q23)
6125	cg43985169	958	ACTGCTAAATTC AGTTTACGAGAG G[C/A]ATTGTGTG GCTGCTCAATTA ATGTA	C	A	Ala	Glu (8296)	NON- CONSER VATIVE	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	

6126	cg43949555	217	CCACTCGTACAG CATATGGACCAA ATTAJGGAATGAA CAAAATGGTTAT CAACC	T	A	Asn	Lys (8297)	NON- CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa.pcls:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6127	cg43949555	858	ACAGTGTGATA AAGAATGCTGAA ATTAJATTGATGA ATTTAGTAAGG GAGAA	T	A	Ile	Lys (8298)	NON- CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa.pcls:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6128	cg43984905	1866	GGGCCAGAGAT GGACGTGTACCA GGAGJCCGCTT CCAGGACAACG GGGCCTGT	A	G	Asp	Gly (8299)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6129	cg43984905	2088	ACAGTGGAGATC CATGGCGTGAG CC[G]AGGACGT GGCCAGCCGCC AGACTGCT	G	A	Arg	Gln (8300)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3

6130	cg43984905	2262	TTCATTGGCCAG AGTACCATCCCC TTT/GJGAACAGCC TCAAGCAAGGAT ACCGC	T	G	Leu	Trp (8301)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6131	cg43984905	884	TGAGCGCTACGA GCCCAGCGGAGA CTG/AJCCAAGG CGCAGCGGCAG ATGACCAA	G	A	Ala	Thr (8302)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6132	cg44011461	2013	GTAGAGGGAGTT TATATCTCTTCC [A/G]TATTGTAGC GCTCCAGGAGCT CGGG	A	G	Met	Thr (8303)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0 (16q24.1 )	16
6133	cg44011461	2420	GGTAGTGCTGGA TGAGGGCATAGA TTG/CJCTGCTGAA GGTGAGGTTGTC AGTCA	G	C	Ser	Arg (8304)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0 (16q24.1 )	16

6134	cg44011461	2423	AGTCTGGATGA GGGCATAGATGC TIG/CJCTGAAGT GAGGTGTCACT CAAGT	G	C	Ser	Arg (8305)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0	16 (16q24.1)
6135	cg44011461	963	AACCGTCGCTT GAACCTGTTGT G[C/T]CATACTCG GCTCCACAGATC TCCAC	C	T	Gly	Asp (8306)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0	16 (16q24.1)
6136	cg42031001	362	CCCGCTGCCACT GATAGGAACCT A[G/T]AGGCTCCA GCAGCAGACAG AGCAGC	G	T	Arg	Ile (8307)	NON- CONSER VATIVE	fgf	Human Gene Homologous to SWISSPROT-ID:P12034 FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5) - HOMO SAPIENS (HUMAN), 268 aa.	6.1E-141	4
6137	cg43320667	824	TTGCTGGTGGAG CTGCCCGCCTG GG[G/C]CTGCTC AGGACCAATTCTC TGGCGGA	G	C	Pro	Ala (8308)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0	3 (3p25)
6138	cg43320667	825	TGCTGGTGGAG CTGCCCGCCTG GG[G/C]GTGCTC AGGACCAATTCTC TGGCGGA	C	G	Gln	His (8309)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0	3 (3p25)
6139	cg43320667	853	CTCAGGACCATT CTCTGGGCGAAC G[A/G]TGCTCTCG CTGGGCTGGAC CATGAC	A	G	Ile	Thr (8310)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0	3 (3p25)

6140	cg43286057	1828	GGGGGGCATGC TGCTAATCGACC TGT/GIGTATCCT GATCTACTGGCA GGTGT	T	G	Cys	Gly (8311)	NON- CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
6141	cg43286057	1841	CTAATCGACCTG TGATCCTGATC TIA/GICTGGCAG GGTGTGGAACC CCTGCCA	A	G	Tyr	Cys (8312)	NON- CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
6142	cg43969076	1020	ACACATCTGCAT CACTTCCTCTGC A/G/TAGGGGTA GTGGCTGGTAC GGAAAGC	G	T	Ser	Tyr (8313)	NON- CONSER VATIVE	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0 (7q21.11)	7
6143	cg43969076	237	TGGTATCAGTCT TGCTCAAGTAAA C[G/A]GGCTGTTT TCCAAACATTGT GACTT	G	A	Pro	Leu (8314)	NON- CONSER VATIVE	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0 (7q21.11)	7
6144	cg43969014	688	ATCACCATCCTC CCACGAGTACAG G/T/GJAGGCGGG GTGTTCTGTGCAT CAGGTA	T	G	Tyr	Ser (8315)	NON- CONSER VATIVE	glucuronidase	Human Gene Similar to SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.4E-80	5
6145	cg43285373	12871	TCTGCCTGGATG AATGGAGAGGAC C[G/C]CAACATCC TGGTTTTCGAGG ACCTT	G	C	Arg	Pro (8316)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P98164 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) - HOMO SAPIENS (HUMAN), 1751 aa (fragment).	0	2

6146	cg43286488	1356	CTCCAGGTAAGT A ATGAGTGACCCAC A[A]GJGTGCCCG AGAGATCAGGGT TCCACT	G	Leu	Pro (8317)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. pcls:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0	12
6147	cg43943531	1467	CAGGATTCCACC A TACCCTATTAAAG A[A]TJGAAGTGG CAAGTGGGATGA TACTG	T	Asn	Ile (8318)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6148	cg43943531	504	TCCTTCACGCC A ATCGTCACGTAC C[A]TJCCTTACCA AAGAGCTCAAGG ATGCA	T	His	Leu (8319)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6149	cg43943531	861	TACTGCCTGGC T ACTATACCTTCTA [T]/GJGCAGATCTC CTTTGTGGGTTT CCAG	G	Met	Arg (8320)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6150	cg43065490	1172	ACTATAATGAGG G AGGACTTCAGA A[G]CJGGAGAAG GCCAGAGAGGC AGAATCT	C	Lys	Asn (8321)	NON- CONSER VATIVE 1096	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)



6151	cg43065549	1598	GGTTATGATGG ATGGCAGATTCT C[G/C]ACCCAAG TGCTCCTAATGG AGGTGG	G	C	Asp	His (8322)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6152	cg43065549	1738	CCATAAATGCCT CATGTGTGGTCT G[G/A]AAGTGCT GTGAGGATGGG ACACTGG	G	A	Trp	End (8323)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6153	cg44034764	1079	GTGCTCGGGCC AAAGGCCTCAGG AA[A/C]AAACAAA GCCGCCAGCGT GGGCTCG	A	C	Phe	Val (8324)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6154	cg44034764	266	CTGAGGGGCC GTGGACTCGGA GGT[G/T]TGGAG GGCTGTGAGTGT CGTGAGAG	G	T	His	Asn (8325)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6155	cg43997653	1941	CAAGCGCCATGT CTTCCACTTCGG C[A/G]CCGTGAG CCCCAGAGCCTC CCAGGC	A	G	Thr	Ala (8326)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa.	0	
6156	cg44004239	391	GAAGACCCAAGT TACCCATCCTGG G[G/C]TGAGTGC CCACCTCAGAAAG TCAAAAT	G	C	His	Gln (8327)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	

6157	cg43010733	1380	GAGCCCTTCGCC TTCCACATGCCG A/A/C/GTCGCTCT ACGGCTTCTTCT GGAAG	A	C	Lys	Thr (8328)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (GNT-III) (GLCNAC-T III) - HOMO SAPIENS (HUMAN), 531 aa.	5E-304	
6158	cg43094362	191	CCCACTGCTCTA CTTCATGGTCAC C/A/C/CTCCTGTC CAGGAAGATCAG TGGCC	A	C	Ser	Arg (8329)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6159	cg43094362	271	ATGCCTGCGGTT ACGGGAAGCAG AC/G/CTGGACC ACTGGCTCACGA CACGAGG	G	C	Thr	Arg (8330)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6160	cg43094362	287	GAAGCAGACGT GGACCACTGGCT CA/C/T/GACACGA GGCTGCCTCCTG GAATGG	C	T	Val	Met (8331)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6161	cg43987514	963	CTAGCGCAGAGA GTTCTGGCCG CT/G/C/CTTCCGC TGGCCCCCAGT GCCCCAG	G	C	Ser	Arg (8332)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	

6162	cg43301245	866	GGCATAGGGGA CCTGCTGGCCG AGG(A/G)TTCTAT GGACTGTGGCTC CGCGGAG	A	G	Ile	Thr (8333)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
6163	cg43074195	2209	GACCCCAAGCA GCACCACCACAA CTC(A/JAAATTAC CAAGACTGTAA AGGTGG	C	A	Gln	Lys (8334)	NON- CONSER VATIVE	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.4E-197	1
6164	cg43988092	2155	AGGCGGGAAT GTGGAAGAA TTT(C/JAACAAAA TAATGTAGCACC AGAAGA	T	C	Lys	Glu (8335)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
6165	cg42671047	1163	ATCATCCTCTAC TGGGGACACCA CTT(C/JTTCCATG AATTGGATTGCC TTGGTA	T	C	Phe	Ser (8336)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P29017 T- CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.lpcis:SWISSPROT-ID:P29017 T-CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.	2.8E-184	1 (1q21)
6166	cg43991224	193	AGGCAGGTGATC AGGATGCCCTTC TTC(G/JTCATCTGT CTACCTACAGCC TGGTT	C	G	Ser	Cys (8337)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.5E-139	

6167	cg43991224	297	GGATGAAAGAGAC GCAGCTGTACAC A/C/A/CTGCTTCC TTAAATGCTCT CTGCA	A	Pro	Thr (8338)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.5E-139	
6168	cg43076975	1728	TAACAATGCATT TCAGCTCGTCAG C/A/T/TGGGAAG CTGTCCATTGAA AAGGC	T	Ile	Phe (8339)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa. lpcis:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa.	3.4E-120	5
6169	cg43924574	470	TAGGGAACCTGC TGATCCTGGAGC C/G/A/CGTGATCT TGGCTCCTTTCA GGAAC	A	Arg	Trp (8340)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1E-106	1

6170	cg44929742	869	CAGGGTCAGCC GGTACATCTGGG CC/T/GJGGGCAT TGGGCTCCAGC CGAAGCAG	T	G	Gln	Pro (8341)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa.   pcis:SWISSPROT-ID:P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa.	5.4E-94	19
6171	cg44021513	1356	TTCTGGCCCTGC TGGTACGCGGG GG[C/G]GTCTGC GCTCCTGCTGAA CTTCACT	C	G	Ala	Pro (8342)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
6172	cg43983795	1531	TACGGCCCTCG GGCCCGTAGAAT T[C/T]GCGGCCTT TGGTCACATCGA ACACC	C	T	Glu	Lys (8343)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q96250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.2E-74	X
6173	cg41568631	1756	GCACCCAGAAG GCTCAGACGCA GAG[C/G]GGAAG GCAGTAGAGACA GCAGCAGC	C	G	Arg	Gly (8344)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.9E-70	14 (14q11.2)

6174	cg41568631	1757	CACCCAGAAGG CTCAGACGCAGA GC[G/C]GAAGGC AGTAGAGACAGC AGCAGCC	G	C	Arg	Pro (8345)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.9E-70	14 (14q11.2 )
6175	cg42659724	773	ACTTTACTAAAA GCTTATTTCTGT C[AT]ATATCAT TTTGTAGAAATC ATCCA	A	T	Gln	Leu (8346)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P26717 NKG2-C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa.lpdls:SWISSPROT-ID:P26717 NKG2- C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa.	1.8E-69	
6176	cg43918233	1027	TC TTCAGAGCCT ACTGAGGATGTG G[AG]GCCCAAA GAGGCTGAAGAT GATGAT	A	G	Glu	Gly (8347)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
6177	cg43918233	534	CAGCCCCAACAG GTCGGGTGCGG AG[G/C]CAAAGA CCCAAAAAGACA GCCCTAG	G	C	Ala	Pro (8348)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
6178	cg43078615	248	CTGTCCGGCGCT GCCTGCCCTCT G[G/C]GCCCTAA CACTGGAAGCAG CTCTCA	G	C	Trp	Cys (8349)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to TREMBLNEW- ID:G2909819 ERYTHROCYTE MEMBRANE GLYCOPROTEIN RH50 - HOMO SAPIENS (HUMAN), 409 aa.	7.1E-60	1 (1p36.2)
6179	cg44913214	2075	AAGCTGTTGAAT TTGGAGGGCTTT C[CT]ATCAGGGA GCCAGTCACGAT TGTCAT	C	T	Pro	Leu (8350)	NON- CONSER VATIVE	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0	10

6180	cg43956596	3949	CCGGAAGAGC AAGGGAGCCC ATG A G CCCCCTC GCCGCACGCCA GCCCGCTT	A	G	Thr	Ala (8351)	NON- CONSER VATIVE	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
6181	cg43916626	2264	CTCTCTGTGAAT CTGGCTGGCAA GT A T GTCGTGT TGGTGATATAAT CAGGGC	A	T	Leu	Gln (8352)	NON- CONSER VATIVE	helicase	Human Gene Homologous to SWISSPROT-ID:P45818 ATP- DEPENDENT RNA HELICASE ROK1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 564 aa.	4.8E-103	17
6182	cg43971940	930	GATTGTGTAGCC ACCTCCTCCAAG CT A T CAGTAAT GGTAAGTTAAA GTTT	T	A	Lys	Met (8353)	NON- CONSER VATIVE	histone	Human Gene SWISSPROT-ID:Q92769 HISTONE DEACETYLASE 2 (HD2) - HOMO SAPIENS (HUMAN), 488 aa.	2.5E-176	6
6183	cg42341753	1486	GGCGAGAAGCC ATCAGGTGGAGC CC C T GGCTGC GGATGGCGAGC AGGACGAG	C	T	Pro	Leu (8354)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:Q14774 HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa.	5.2E-263	1
6184	cg43332152	982	CCTGGCGGCCA AGCGGCGGGGA CCG C G GCACC ACCATCAAAGCC AAGCAGCT	C	G	Arg	Gly (8355)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17
6185	cg41637704	1202	GGAGCTGCTGG GGCCGCCAGCG CCG C G GAGAC AAGGCAGCGG ACCGCCTGC	C	G	Arg	Gly (8356)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7

6186	cg43143467	630	CTTGCCAACGTA CCAGCTGTGCGA G/A/CJCCCTCTTAC CAGCCCACATCT ATTCC	A	C	Thr	Pro (8357)	NON- CONSER VATIVE	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6187	cg43143467	631	TTGCCAACGTAC CAGCTGTGCGA G/A/CJCTCTTAC CAGCCCACATCT ATTCCA	C	A	Thr	Asn (8358)	NON- CONSER VATIVE	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6188	cg42721526	769	GGGTCTCTTGCC CATCTCTCCGGC C/G/AJCCCCGCC AGGAAACGACGA GAAGGC	G	A	Ala	Thr (8359)	NON- CONSER VATIVE	homeobo x	Human Gene Homologous to TREMBLNEW-ID:G2822175 HXA1_HUMAN HOMEOBOX PROTEIN HOX-A1 - HOMO SAPIENS (HUMAN), 335 aa.	6.9E-144	7
6189	cg42359655	4927	CCTATTTTCAAG AATGGAGATTAC A/G/AJTGAGGTG ATGAAGACGCG GATCCGT	G	A	Ser	Asn (8360)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLCERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)
6190	cg43296921	553	AGCCGCCCTGGC TCATTCCTTCTC CTT/GJTCAGGTT AACAGAGAGGTT GATGTC	T	G	Lys	Thr (8361)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.3E-238	15 (15q23)
6191	cg43927025	192	GTTGGTGGTCTG TTTGGTTCTCTG G/A/CJCCCTGCAT TCTGAGGGGTCT GGAGG	A	C	Thr	Pro (8362)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.1E-224	10 (10q24)



6192	cg43927025	213	CTGGACCCTGCA TTCTGAGGGTC T[G]A[GAGGGAA ACTGACAGCTGT GGATCC	G	A	Gly	Arg (8363)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.1E-224	10 (10q24)
6193	cg43285385	621	ACATTGAAAAAC TTCITTAACITTT IC/TTATTCATTGT AAAATTCTTCAC GGAG	C	T	Glu	Lys (8364)	NON- CONSER VATIVE	hydrolas e	Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.8E-173	8
6194	cg43925670	1254	GCCTCTGAAGGA TATGGAAGCTGA CT/GICTGTTCCT GGGTAGCTTCA TGCTC	T	G	Ser	Arg (8365)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1

6195	cg43925670	438	CCACTTTTCGGT GCCAATTCAAAG C/A/TGGTGAGTT TCAGTTTATCTC CTTCC	A	T	Cys	Ser (8366)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.   pcis: SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
6196	cg43925670	479	ATCTCCTTCCTC ACAGTTGATTGT G/G/TTCAGTCGT CCATGCACCACC ACTTC	G	T	Thr	Asn (8367)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.   pcis: SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
6197	cg43082514	349	AAAAGATGCACC ACTCTTTAGAAA C/T/CjGGGCAAT CCATACAGGAAA GCATCA	T	C	Trp	Arg (8368)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.5E-188	4 (4q35.1)
6198	cg43925658	578	TGAAATTCCTGA AACCGACCATAG T/G/AjGAAATGTA TGTCCTGCATTG TTTCT	G	A	His	Tyr (8369)	NON- CONSER VATIVE	interferon	Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa.	4.8E-141	10 (10q23)

6199	cg43972852	849	TTCACATCTCAC TAACAAGTTTGA GIGTTACAAGACT GTGGCATATACA GAGCA	G	T	Asp	Tyr (8370)	NON- CONSER VATIVE	isomerase	Human Gene SWISSPROT-ID:P30101 PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (GRP58) (ERP57) - HOMO SAPIENS (HUMAN), 505 aa.	3.8E-274	
6200	cg44929725	2694	ATTGAGAAAGAG AGATTCTATGAA AIA/GJCCGGTGC AGCCAGTGACA CCATCA	A	G	Asn	Ser (8371)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6201	cg42859664	747	GGTCCACTTCAC GGGACTTGCTCT GIA/GJGGCCCCC TGAGGCTGCATA GACCCC	A	G	Leu	Pro (8372)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0	15 (15q26.1)
6202	cg42859664	748	GTCCACTTCACG GGGACTTGCTCTG AIG/AJGCCCCCT GAGGCTGCATAG ACCCCA	G	A	Leu	Phe (8373)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0	15 (15q26.1)
6203	cg43917392	3326	ATTTGTCTCACT GGGTACTAACAG AIC/ITAAAGGAT AGAGCGTAGTGA CTAAT	C	T	Ser	Asn (8374)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P34925 TYROSINE-PROTEIN KINASE RYK PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 604 aa.	4.0e-315	
6204	cg43957153	329	TGAGGAGGGGG AGCTGAGAGATC ACIC/ITGCATGGA GATCACAAATAAG GAACCTC	C	T	Arg	Cys (8375)	NON- CONSER VATIVE	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.2E-304	4 (1p36)
6205	cg43962792	1126	CCGCGAGAGTG AAACCACCAAAG GTG/ITCCTATTC ACTTCTATCCG TGATTG	G	T	Ala	Ser (8376)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P08241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.3E-300	6 (6q21)

6206	cg43965549	1355	GCCAGAGAGG ATCAGCCACGCT GTTC/AJAGAGTCT GGACTCTGCCCT CTTGGA	C	A	Gln	Lys (8377)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE - SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
6207	cg43965549	1356	CCAGAGAGGAT CAGCCACGCTGT CIA/CJGAGTCTG GACTCTGCCCTC TTGGAG	A	C	Gln	Pro (8378)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
6208	cg43967889	1158	GAATTACGGGAC CCAAATGTCAAA CTT/AJACCAAATG GGCGAGACACA CCTGCA	T	A	Leu	Gln (8379)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.9E-226	3
6209	cg43967889	663	ATCTGCCATCGG GATATTAAACCG CIA/GJGAACCTCT TGTTGGATCCTG ATACT	A	G	Gln	Arg (8380)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.9E-226	3
6210	cg43963232	2187	AGTACTGTCCCC GCGAGCATCGA GGJ/GJATTCTA CTGCACCATCT CTTCCA	G	C	Ile	Met (8381)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P31323 CAMP-DEPENDENT PROTEIN KINASE TYPE II-BETA REGULATORY CHAIN - HOMO SAPIENS (HUMAN), 417 aa.	4.6E-223	7 (7q22)
6211	cg43947829	1933	ACAGGTAATGGA TTCTGACAAAGGA ATT/ATTGCTGAG TCACGAGAACAC GTTTT	T	A	Ile	Phe (8382)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	

6212	cg38438124	850	ATGGGATCACCC TTCAACCCAGT TIG/CIGTGGCA TGTACCGGCTTA ATGTTG	G	C	Leu	Phe (8383)	NON- CONSER VATIVE	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.8E-216	10
6213	cg43917871	1966	TCAGCCAAACCC CAGTCTATTAGT CIG/ATAGCTTTC TGTGCTCATGAT CAATC	G	A	Arg	End (8384)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
6214	cg43933472	2482	TTTCATTGCTC GATGGTTGGTGC TIC/TJGAATAATG TCATTGATTCCA ATGAT	C	T	Arg	Gln (8385)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
6215	cg38309035	487	TGCAGGGACTC GAAGTAGGGATG GG[C/A]CAGCGC CTCGCCTGCCGT CACCCGC	C	A	Ala	Ser (8386)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P53778 EXTRACELLULAR SIGNAL- REGULATED KINASE 6 (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-ACTIVATED PROTEIN KINASE-3) (MITOGEN- ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP KINASE P38 GAMMA) - HOMO SAPIENS (HUMAN), 367 aa. lpcis:SPTREMBL-ID:Q99588 STRESS-ACTIVATED PROTEIN KINASE-3 - HOMO SAPIENS (HUMAN), 367 aa.	2.9E-195	

6216	cg43929069	347	AGTAATTCITTTG GCTGGATCATAC TTCJCCAACATTT TCTGAATGAGGT CAAA	T	C	Glu	Gly (8387)	NON- CONSER VATIVE	kinase	Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa. Jcds:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.	1.6E-192	
6217	cg43007055	693	CGGAGCGGGG CGCGTCGCCC TCCGTCGCGCC GAGAAAGGTGA GCCGGCCGC	G	T	Ala	Ser (8388)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
6218	cg43007055	798	AGCGAGGCTG CCGAGCCCGGC TCGTCGJCCACG GCCGCGGAGGG AGAGGCCGC	C	G	Pro	Ala (8389)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
6219	cg43982923	912	AGTTGCAATGGT GACCTCGATCCT GATJGATTGTAA AGTCATTCTCT TCCAG	A	T	Glu	Val (8390)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
6220	cg43989473	2576	GCCTCCCAGCAT TGGCAAATCGAA CIGATJGGACAG ACGTCAGGCAGA AATTGG	G	A	Val	Met (8391)	NON- CONSER VATIVE	kinase	Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.1E-154	11
6221	cg44016530	539	ATGCTGAACATG CTTCGTGGGGCT ATATCTTTTGT TTCTCTGTAGTC TCITT	T	A	Asp	Val (8392)	NON- CONSER VATIVE	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12

6222	cg43286014	257	GAGCGAGGGCG TGACGCTCGTCG TGTTGACAGATA AGCTTGTTCTGG TGTTGGC	T	G	Tyr	Asp (8393)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSPROT- ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa.	1E-87	
6223	cg43984445	308	TTACCTCTCTCA TGAGGTCTTCTT GTATTTGGTTAC TTCCTCAGAAAA ATCAT	T	A	Lys	Asn (8394)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSPROT- ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.13) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa.   pcds:SPTREMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.13) - HOMO SAPIENS (HUMAN), 277 aa.	8.7E-73	2
6224	cg43985883	186	AGTCACAAGCGG AAGAGGAGATCT CAGAAAGGAGC ACACAAGAGAAC AGGAAT	G	A	Arg	Gln (8395)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa.	1.2E-64	
6225	cg43985883	226	AGAACAGGAATT GTATACCACATC AAGCTGTGTTAA ACAATCTGATTG TGCTC	G	C	Gln	His (8396)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa.	1.2E-64	
6226	cg43982810	227	GGACCCAAACAT CATCCATCTATT AAGTTCTGTGTGT ATCACTGATGAC CCTCT	G	T	Ala	Ser (8397)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:Q16832 RECEPTOR PROTEIN-TYROSINE KINASE TKT PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE TYRO 10) (NEUROTROPHIC TYROSINE KINASE, RECEPTOR- RELATED 3) - HOMO SAPIENS (HUMAN), 855 aa.	0	1

6227	cg14396889	1094	CAATCAGCTTTG GTTACCATCGTA GIA/GJAAAGGGA TTTATAAATGCTA CCAAT	A	G	Glu	Gly (8398)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P36888 FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR FLT3) (STEM CELL TYROSINE KINASE 1) (STK-1) (CD135 ANTIGEN) - HOMO SAPIENS (HUMAN), 993 aa.	0	13
6228	cg44021449	2713	GAAGATCTACAG TGGGGACTACTA TTC/TGTCAAGGC TGTGCCTCCAAA CTGCC	C	T	Arg	Cys (8399)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0	15
6229	cg43322545	1212	GGAGGGAGTGC CCCTGGGCCCC CCT[GIA/JAGAACA TTAGTGCTACGC GGAATGG	G	A	Glu	Lys (8400)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.   pcds:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1 )
6230	cg43991478	1301	AGTAGGTCCGAC GGCCGGTGAGT CC[G/C]GGTTCA CAGTCAAGACGT CAGCAAG	G	C	Pro	Arg (8401)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
6231	cg43991478	1895	GTGCTCCACGTA CTCTGTCAACCAT G[A/C]TATTTTCA GGGCCGCGCAG ACAGAC	A	C	Ile	Ser (8402)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	



6232	cg43991478	894	GCGGCTAGGTCT CGGTGGATGTAG TGCCTGCGCG TGCAGATAGGCC ATGCC	G	C	His	Asp (8403)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	0
6233	cg43991478	895	CGGCTAGGTCTC GGTGGATGTAGT GCGTGGCGGT GCAGATAGGCCA TGCCCT	C	G	Gln	His (8404)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	0
6234	cg43920644	2056	TGACATTCCAAA GTAGCCCGAAAT TTTCJTITTAATCA TTCGGGCAAAT CCCAG	T	C	Lys	Glu (8405)	NON- CONSER VATIVE	kinesin	Human Gene SPTREMBL-ID:Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa.	0	1
6235	cg43942537	1165	CACTGTCTCTTC CAAAACCTTCAC GCTCTCTGCTT GCTTGTCTCGT CTATC	C	T	Gly	Asp (8406)	NON- CONSER VATIVE	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. pcls:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10
6236	cg43942537	1250	TTTTCTGATCT GTGGCTTTCAAC TTCCTCATGTT CTACTCTTAGAC GTTCC	C	T	Glu	Lys (8407)	NON- CONSER VATIVE	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. pcls:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10
6237	cg43964874	3378	ACCAGTGCCACT GTGATCCAAGCA GCTGGGCAGT GCCCATGCCTCC CCAATG	G	T	Arg	Ser (8408)	NON- CONSER VATIVE	laminin	Human Gene SWISSNEW-ID:P55288 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa. pcls:SWISSPROT- ID:P55288 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa.	0	3 (3p21)

6238	cg43983535	2722	TTTGTGTCAAA GTATGTTCTCC C[C]ATGTCAGCC AGTGAATGTAAT CACACG	C	A	Arg	Met (8409)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
6239	cg42536982	7509	CTGCATTGAGCG TTCTAATGCGTT G[C/G]AAGCGAA GGCGAATATATC GTGCAG	C	G	Leu	Phe (8410)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa.	0	
6240	cg44009224	64	GGTCAGCTGCA GCATGGGATGG CTG[A/T]GGATCT TTGGGGCAGCC CTGGGGCA	A	T	Arg	Trp (8411)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0	
6241	cg42930646	1215	TCGTCAATGTTA CTGATCGGATA G[C/G]GTATGGA TGGAAATGGACG ATGAGG	C	G	Ser	Arg (8412)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa.	1.8E-198	1

6242	cg43958558	451	TGAAGTGGTCAGT GTTCAACCAGTA CTTATGTATTTT GAATGGTTTCCC ACTTT	A	Gln	His (9413)	NON- CONSER VATIVE	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.9E-139	14 (14q21)
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6243	cg43958558	762	GGCCAGTGGC AGGCTAGGCTC CGG/GTGGCAC TTGGCTGTCCAG AAGATGGG	G	T	Pro	Thr (8414)	NON- CONSER VATIVE	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.   pcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.9E-139	14 (14q21)
6244	cg43931460	732	AGGTCAGGATTT TGCAGGTCCACT G[A/C]CAGGTGA AGGCGAGTCCG GCCATTA	A	C	Ser	Ala (8415)	NON- CONSER VATIVE	MHC	Human Gene Similar to SWISSPROT- ID:P25963 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3 - HOMO SAPIENS (HUMAN), 317 aa.	7.6E-69	14
6245	cg43111577	1062	AGCCACACAGGG TACAGAGGTGGT TC[G/C]AGCTTAT GAAGAAGAGAAC AAAGCT	G	C	Arg	Pro (8416)	NON- CONSER VATIVE	misc_cha nnel	Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
6246	cg40367355	647	TTTATTCATGGG GACTTAGAACCC G[G/A]TGAGCCC ATTCAAATCATA CCCCC	G	A	Gly	Asp (8417)	NON- CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.1E-199	21

6247	cg44929972	1119	TTCTCTTTGAATT GGCCAGAGGAA TTA/GIGAGAGTG ACTTTTTTATGA AGACA	A	G	Ile	Met (8418)	NON- CONSER VATIVE	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
6248	cg39307062	350	GCAAGATCGACA AGACGCAGCGC AA/G/CJCGCTGT CCCTTCTGCCGC TTCCAGA	G	C	Lys	Asn (8419)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:Q13285 STEROID HORMONE RECEPTOR AD4BP (STEROIDGENIC FACTOR 1) (STF-1) (SF- 1) (FUSHI TARAZU FACTOR HOMOLOG 1) - HOMO SAPIENS (HUMAN), 461 aa.	7.2E-257	
6249	cg43315956	3132	GTGTTACACCTTT GCCAACCAGCTC C/T/AJGCCCTTGG AAATGGATGACA CAGAA	T	A	Leu	Gln (8420)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
6250	cg43315956	3422	AATGCCACCTCT CATTCAAGAAAT G/C/AJTGAGAAAT TCTGAAGGACAT GAACC	C	A	Leu	Met (8421)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
6251	cg43935583	1345	TCAGTATGGCTC TTTTCCAGGTGG C/T/CJTCTCTGGG GGAATGCCTGGT AATT	T	C	Phe	Leu (8422)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6252	cg43935583	1383	TGCCTGGTAATT TTCCCGGAGGAA TTG/AJCTCTGGAAT GGGAGGGGGCA TGCCTG	G	A	Met	Ile (8423)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6253	cg43935583	1411	TGGAATGGGAG GGGGCATGCCT GGA/AJGTGGCT GGAATGCCTGGA CTCAATGA	A	G	Met	Val (8424)	NON- CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22

6254	cg43935583	1527	ATGTGGCTCAGA ACCCAGCAAATA T[G]ATCAAAATA CCAGAGCAACCC AAAGG	G	A	Met	Ile (8425)	NON- CONSER VATIVE	nud_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6255	cg43935583	1577	GTTATGAATCTC ATCAGTAAATTG T[G]GJAGCCAAAT TTGGAGGTC AAG CGTAA	C	G	Ser	End (8426)	NON- CONSER VATIVE	nud_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6256	cg43949686	1320	CCGCGCCCAACC CACCATCTCCAA CC[A]CJGCCTCA CCTCATCTCCTC TGCCAAG	A	C	Gln	Pro (8427)	NON- CONSER VATIVE	nud_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
6257	cg44926604	811	TCTAGTGGCGCG TCAGCTCACAGC T[G]TCTCAAATG GGAACAGATGG GAAGCT	G	T	Gln	Lys (8428)	NON- CONSER VATIVE	nuclease	Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa.	0	3
6258	cg43952559	268	AGCCAGGATTGC CTTCTCCTGCTA T[G]AJATTCCAAA AAATTGGCCTTT AATAG	G	A	Met	Ile (8429)	NON- CONSER VATIVE	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL YPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.8E-156	

6259	cg43952559	765	CAAAATTACTA GGGACATTAAAT TTAGGATATGAC CTGCTCTAGGCA TTCCT	A	G	End	Trp (8430)	NON- CONSER VATIVE	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.8E-156	
6260	cg44130572	604	TAATGAGAACAA AGTTACAACATA CTTCJAGAGCCTC TGGACATAGCTA AGACA	T	C	End	Gln (8431)	NON- CONSER VATIVE	nuclease	Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa.lpcis:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa.	2.4E-53	
6261	cg43951535	1536	GTGAACTACAGC GAGTAGCTTTTA G[C/G]CCTTTGCT TGGGCAAAACCTG CTGAT	C	G	Ser	Arg. (8432)	NON- CONSER VATIVE	nuclease inhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)

6262	cg43988571	2468	GCCTCTTGACCT CACTTGCAGCAC C/A/TJAGGTGAAG ACCTTGCTGCTA AATGC	A	T	Lys	End (8433)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.pcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0	10 (10q24)
6263	cg43988571	2469	CCTCTTGACCTC ACTTGCAGCACC A/A/TJGGTGAAGA CCTTGCTGCTAA ATGCT	A	T	Lys	Met (8434)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.pcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0	10 (10q24)
6264	cg36524555	192	AAGAGCTCTGGG GCCGGGGCGG CA/G/CJGGGCTC CGGGGGCTCGG GTTCCGGT	G	C	Arg	Thr (8435)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681. PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3)
6265	cg36524555	600	GAGAAITCTCAG CCTAGGCGAAAC C/C/TJAACCAAAC TGTCCTCATCT TCAGC	C	T	Pro	Leu (8436)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3)



6266	cg36524555	663	GAACTAAAAGGA ATCTTTCCAAGT G/A/G ACTCTTTC AGGGAGACACAT TTCGG	A	G	Glu	Gly (8437)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3 )
6267	cg44012756	2030	GGCTACACAGG GAGCATGTGTAA CA/T/G CAACATC GATGAGTGTGCG GGCAAC	T	G	Ile	Ser (8438)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6268	cg44012756	2323	CACCTGCAAAGA CATGACCAGTGG C/T/A ACGTGTGC ACCTGCCGGGA GGGCTT	T	A	Tyr	Asn (8439)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6269	cg44012756	559	TGTCACACGAGTG TGGCCAGAAGC CC[G/A] GGCTTT GCCGCCACGGA GGCACCTG	G	A	Gly	Arg (8440)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6270	cg43966629	5250	AAC TTCGGGATC CTGCAGAGGTTT G/G/T TCCTGTG ATGCGTTGTGGA GGTGG	G	T	Thr	Asn (8441)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.3E-123	1
6271	cg43966629	5251	ACTTCGGGATCC TGCAGAGGTTTG G/T/G TCCTGTGA TGCCTTGTGGAG GTGGT	T	G	Thr	Pro (8442)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.3E-123	1
6272	cg43297056	944	GGCAGTGTGGA CATCATCAGCTT CA/C/T ATCCTCA TCCACAATGTCA AGAGCC	C	T	Val	Met (8443)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103	20 (20q13.1 )

6273	cg42904626	196	GTGCCTTGACGA TACAGCTAATTC A/GCJAATCATTT TGTGGACGAATA TGATC	G	C	Gln	His (8444)	NON- CONSER VATIVE	oxidase	Human Gene Similar to SWISSPROT- ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.1E-97	12
6274	cg44028217	428	AACTGCTCAAAG ACCACGGGCGG GTG/CJCCAGGG GTCGTTCTGGTG GTAGATG	G	C	His	Asp (8445)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	7 (7q31)
6275	cg44028217	569	GGCAGCACCTG GTCGGCCATGG AGT/A/GJGATCTG CAGGCGGTACT GCGCTTGT	A	G	Tyr	His (8446)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	7 (7q31)
6276	cg44028217	691	GCCTGGCGCTC CCAGGAGTACTG CGT/CJCTGCTCC AGAGTTGGCTGG ACCACG	T	C	Thr	Ala (8447)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	7 (7q31)
6277	cg43972840	945	GAGGGCAGCAG CTGTCCCTCCG AA/CJAAGCTATG GCTGTGCTGAG GAAGCCC	C	A	Thr	Lys (8448)	NON- CONSER VATIVE	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168 (16p13.3 )	16

6278	cg43948682	1212	AAGTCCTATTCTC GTCTCAGGGACT G[A/G]CGCGTAG TGAATGATGGCG CCGTG	A	G	Ser	Pro (8449)	NON- CONSER VATIVE	peptidase	Human Gene Similar to TREMBL-NEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDOFFER (LYME DISEASE SPIROCHETE), 592 aa.	5E-75	10
6279	cg42347730	1427	TAGTCCCTAAAG GTGATAATCTGC A[C/T]GAAGGCTC CCAGGATTTCC GGGCT	C	T	Val	Met (8450)	NON- CONSER VATIVE	peroxidase	Human Gene SPTREMBL-ID:Q13408 SALIVARY PEROXIDASE - HOMO SAPIENS (HUMAN), 712 aa.	0	17
6280	cg41626506	1001	CTCCAGGCCCTCC AGGTTTCATGCCA G[T/G]GATGCTGT CACAAAGACTCAA AGTCT	T	G	Thr	Pro (8451)	NON- CONSER VATIVE	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0 (3q26.3)	3
6281	cg41626506	2405	TTCTCACAAGTC ATCTGGCAGTCA G[C/A]CCCTCCC CCGAAGGCAGC TTTGCTG	C	A	Ala	Ser (8452)	NON- CONSER VATIVE	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0 (3q26.3)	3
6282	cg42691989	826	CGGGTGGTTGT GCCTCAGAGCG AAG[C/G]CACATT CTCAATCAGCAC GGCCCTG	C	G	Ala	Pro (8453)	NON- CONSER VATIVE	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101 (14q24.1)	14
6283	cg42535091	1803	GCAGGATTGAAGC AAGAGCAGAAAA G[C/G]AAGAGGA AAGGGCACGAAT ATACAA	C	G	Ser	Arg (8454)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0	12
6284	cg42535091	1840	GCACGAATATAC AAATATTAAGTAT [T/C]CTCTAGCGG ACCAGACGAGTG GAGA	T	C	Ser	Pro (8455)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0	12

6285	cg43920534	4693	GGCTGTTGGCC CACTTGTGGAC C[G/A]TCTCCATA TCACACAGATTG TCCAC	G	A	Thr	Met (8456)	NON- CONSER VATIVE	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0	12
6286	cg43920534	4727	TCACACAGATTG TCCACTAAATC C[G/A]GACATGCTT CTTCTTTACCCC AGTGA	A	G	Trp	Arg (8457)	NON- CONSER VATIVE	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0	12
6287	cg43321833	2318	ACTGACGTGATC GCTGGCCTCCTC A[C/T]GTTACCA TCAATCTCCTGG GGGTG	C	T	Thr	Met (8458)	NON- CONSER VATIVE	phosphat ase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6288	cg43321833	2324	GTGATCGCTGGC CTCCTCAGGTC A[C/T]CATCAATC TCCTGGGGGTG ATGCTC	C	T	Thr	Ile (8459)	NON- CONSER VATIVE	phosphat ase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6289	cg43321833	2330	GCTGGCCTCCTC ACGTTACCCATC A[A/T]TCTCCTGG GGGTGATGCTCA CCATC	A	T	Asn	Ile (8460)	NON- CONSER VATIVE	phosphat ase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6290	cg42460457	1437	GGTCACGTCTAG TGTCAGCTGTGG G[G/A]GCCGTCA CCAGTCTCCTAT TGACAT	G	A	Gly	Ser (8461)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6291	cg42460457	1473	GTCTCCTATTGA CATTTTAGACCA GT/CJATGCCGG TGTTGGGAAGA ATACCA	T	C	Tyr	His (8462)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)

6292	cg42460457	3466	ACCTTCGTGTGC CTCATCCTTCTC ATTCGTGTGTGC TCGTTACTGGA GAGGG	T	C	Ile	Thr (8463)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6293	cg42460457	5419	CAATACCAGTTC ATCTATAAAGCA AIGTGTCTTAGCT TGGTCAGCACTA AAGAA	G	T	Arg	Met (8464)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6294	cg43928335	3499	AGCAAGAGCTAA TAGTACCTCATC TTTATCATCATAA ATTGTATCTGTA AGAAA	T	A	Glu	Val (8465)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.2E-302	11 (11q22)
6295	cg43988365	2003	AACGAGATGTCC AGTTCATACAGT CCTGTGCTCTTAA AGACAGACAAC CCTTG	C	T	Gly	Arg (8466)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa. lncs:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
6296	cg43307302	1279	TTGGTTGGCGCT TTTGTGGCTGG ATC/GACTGTTT TTCAGCAAAATG CCCTA	C	G	Thr	Arg (8467)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	8.7E-218	18 (18p11.3)
6297	cg44004203	3233	TCCATTGTTGCT GATCTGGAACCT CTTCCTCTTTGT AGTTGCCGAAAC TTCAC	T	C	Glu	Gly (8468)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	

6298	cg43269274	1136	TCCTCCATCCCA GTTTACAGGAG TGGTGGCCGT TGCCACAGGGCT TCTGCT	G	T	Pro	Gln (8469)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6299	cg43269274	1137	CTCCATCCAG TTTACAGGAT G/GTGGCCGT GCCACAGGGCTT CTGCTG	G	T	Pro	Thr (8470)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6300	cg43269274	1984	AGCGAGTAGCG AGGTGAGGACG ACA/C/AJGCGG GGCTCTCCTCTC GCAGCTTC	C	A	Arg	Leu (8471)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6301	cg43301213	527	CAGAAATGCATCC CTAAACTCAGC A/G/AJAGAGGCA GTAAGGAACCCA GCACAA	G	A	Glu	Lys (8472)	NON- CONSER VATIVE	phosphatase inhib	Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (L-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
6302	cg44021995	2419	TAAAGTAGTGGA CAGCCTGGCCC CA/T/CJCCATTAG TAATGTTTTAGT GCAGGG	T	C	Ser	Pro (8473)	NON- CONSER VATIVE	phosphorylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. pccs:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0	16

6303	cg44021995	2429	GACAGCCTGGC CCCATCCATTAC TAJ/CJTGTTTTA GTGCAGGGCAA ACAGGTA	A	C	Asn	Thr (8474)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. pcis:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0	16
6304	cg43996195	1215	TGTCACCTTCCA GAGTGGGTACC CTT/CJCATACAT GTGGAACCTGCC CTGCAT	T	C	Glu	Gly (8475)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
6305	cg43996195	1216	GTACACCTTCCAG AGTGGGTACCCT TIC/TJATACATGT GGAACCTGCCCT GCATC	C	T	Glu	Lys (8476)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
6306	cg42688448	1817	GCGCCATGGTA GTCTGAGGCTG GGC/A/CJTGGGC ATGGGCCCTGCAT CTGGGCCA	A	C	His	Gln (8477)	NON- CONSER VATIVE	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
6307	cg42688448	1823	TGGTAGTCTGAG GCTGGGCATGG GC/A/CJTGGGCC TGCATCTGGGCC AAGGCCT	A	C	His	Gln (8478)	NON- CONSER VATIVE	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
6308	cg44022214	2014	TGGAAGCTCACG GCATTGAGCGTG TTA/GJGGAGCGG AGCTTGACTCC CGCAGC	A	G	Tyr	His (8479)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. pcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)

6309	cg43958858	2406	CACAGAAATCCAT CAACCGGGACA GC[G]A/JAAGAGC CCTTCTCTTCAG TTGAGAT	G	A	Glu	Lys (8480)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.lpcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)
6310	cg44016415	1881	AGGCGCATAGG CCCTCTGACTTG CA[A/G]TGAGGT TGATCCATCCTG ACAGAT	A	G	Ile	Thr (8481)	NON- CONSER VATIVE	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
6311	cg43993893	1310	CTCAAAGTTTGC GAGTTCTGTGAG C[A/T]TGTCGGTG ATTCCCCCGTTG AGAGT	A	T	Met	Lys (8482)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
6312	cg43993893	680	CATGAACCTTTGT CTCACCCCTTTGA C[A/C]GGGTATCT GTGATAAAATGA ACCTT	A	C	Leu	Arg (8483)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
6313	cg43916712	3743	TTCTCGGGCTT GGGGTACACTGT GT[G]GCCCTCAG GGCATTGTCTGG ATCGTA	T	G	His	Pro (8484)	NON- CONSER VATIVE	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	



6314	cg43916712	3744	TCCTCGGGCTTG GGGTACACTGTG TGTCTCTCAGG GCATTGTCTGGA TCGTAT	T	His	Asn (8485)	NON- CONSER VATIVE	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
6315	cg42534568	911	ATTAAAGAAGAG GAGAAGCCCCCT GCCTCTCCGCA CGAGTTCCAGCG CCAGGTG	T	Pro	Leu (8486)	NON- CONSER VATIVE	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
6316	cg43262191	1277	GAAGCGCTTTGT TTTCTCTCTACAA TGAJCCATTCCCC GCATAGCTACCA CCAT	A	Ala	Thr (8487)	NON- CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0	3
6317	cg42697980	479	GTTGGGGGCAG GTATGTCACCGT TCGTGTCGTGGA CCACAGTCCCTA GGACACG	T	Arg	Leu (8488)	NON- CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa.lpcis:SWISSPROT- ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa.	5.9E-262	
6318	cg38427250	754	GTTGAGCAATGT GCACTTCACTGA AAGJAGAAAGAA CTGGAATTTGCG TCTGG	G	Lys	Glu (8489)	NON- CONSER VATIVE	protease	Human Gene SWISSPROT-ID:P42575 CASPASE-2 PRECURSOR (EC 3.4.22.-) (CASP-2) (ICH-1 PROTEASE) (ICH- 1L1S) - HOMO SAPIENS (HUMAN), 435 aa.	4.9E-226	7

6319	cg43306871	605	GCGTATGACTTT ATTGATCCAGGA C[A/G]TGATTTG CAGATCTGGGTG TAGAC	A	G	Met	Thr (8490)	NON- CONSER VATIVE	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
6320	cg43074055	584	CCCAGGCCAACCT CAGTGCCTCCGT C[G/A]CCACAGT CCAGCTGCCACA GCAGGA	G	A	Ala	Thr (8491)	NON- CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.7E-138	19 (19p13.3)
6321	cg44031287	393	TGGTTTCACTG ACAGGGGAGAC AC[G/T]AGAGTCA TTGTAGACATGC CAACCA	G	T	Arg	Ser (8492)	NON- CONSER VATIVE	protease	Human Gene Similar to TREMBLNEW- ID:G2736064 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa.	8.1E-67	1
6322	cg35817832	780	AACTTCTAAGCT CACCCGTGCTGA G[G/A]CTGTTTT CCTGATGTGGAC TATGT	G	A	Ala	Thr (8493)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.1E-63	X

6323	cg42914280	434	ATATCTAGAAA CTACTACGACCT C[G]A/JAAAAAGAT GTGAACAGTTT GTTAG	G	A	Glu	Lys (8494)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.   pcds:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.3E-63	11 (11p23)
6324	cg43979831	1346	GCACCGAGGCT GCAGCAGCCAC CAG[C/G]TTCGC GATCAAAATCTT CTCTGCC	C	G	Ser	Arg (8495)	NON- CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.1E-228	14
6325	cg43511784	1247	CTATCCCCCCCCG AGGTCAAGTTCA A[C]A/JAAACCCCTT TGCTCTCTTAAT GATTG	C	A	Asn	Lys (8496)	NON- CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
6326	cg43268468	1080	GGAGGCACCTCTT GAGGTTCTTCTG G[G/C]GGGCAGT GACCGTGTCAAG GAGCTC	G	C	Pro	Arg (8497)	NON- CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188 (17p13.3 )	17
6327	cg43268468	1260	CAGGAGCACGTT GGTCGTGGGC TC[A/G]TGCTGGA TCGCACCCGGTA CAGGTC	A	G	Met	Thr (8498)	NON- CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188 (17p13.3 )	17
6328	cg43932980	261	TGGGAAGTGGT GACACACGGTTA CT[G/T]CGGCTTG GGTGTCGGTGA CCAGCCG	G	T	Cys	Phe (8499)	NON- CONSER VATIVE	protease nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.7E-152	20

6329	cg43060292	1245	TACTACAGAAGG GATGGGTTGACT T[G]/JTTTGTCC AAAGTTTCCATT TCTG	G	T	Leu	Phe (8500)	NON- CONSER VATIVE	protease inhib	Human Gene Similar to SWISSPROT- ID:P09006 CONTRAPIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa.	2.2E-83	X (Xq22.2)
6330	cg44921824	1452	CAGCACCACAGC GTGGTAGGCCTC C[C]/JGCAGCTC CGGCACCCGTCA CGTCCCT	C	T	Arg	Gln (8501)	NON- CONSER VATIVE	reductase	Human Gene SPTREMBL-ID:Q13718 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa.	3.2E-270	
6331	cg44921824	1741	TGTGTGGAGAAA TGGTGGCAGAA GC[T]/CJCGGGT GCTCCCGGCGG GAGGCAGC	T	C	Ser	Gly (8502)	NON- CONSER VATIVE	reductase	Human Gene SPTREMBL-ID:Q13716 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa.	3.2E-270	
6332	cg43941472	771	AGGGGATGTCG CCAAAGCCTTTG GA[G]/AJCTGGAG CAGATTTTGTCA TGCTGGG	G	A	Ala	Thr (8503)	NON- CONSER VATIVE	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184	X (Xq28)
6333	cg43941472	837	TCATACGGAGTG TGCTGGAGAAAT GT[A]/TTGAGAGG AACGGACGGAA GCTCAA	T	A	Phe	Ile (8504)	NON- CONSER VATIVE	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184	X (Xq28)
6334	cg43286949	1008	ACGCCAACTTC CTCTCGGGCTCT GT[C]/ATTTCATCT TGGTCTCTTCCT TCGGT	T	C	Thr	Ala (8505)	NON- CONSER VATIVE	reductase	Human Gene SWISSNEW-ID:P63004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.[pcis:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7

6335	cg43286949	848	GGAAAGAGCATC CTCCAAAGAAAT CTTCJGCTGGACT CCATCAATGCTC CCGAG	T	C	Gln	Arg (8506)	NON- CONSER VATIVE	reductase	Human Gene SWISSNEW-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.   pcds:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
6336	cg43925599	570	GGGTACCTGGAA GAGTGAGCCTG GTTC/AJAGGTAA AGCAGCTGTTAA GTATGC	C	A	Gln	Lys (8507)	NON- CONSER VATIVE	reductase	Human Gene Homologous to TREMBLNEW-ID:G2707824 ALDEHYDE REDUCTASE - HOMO SAPIENS (HUMAN), 325 aa.	5.6E-140	1
6337	cg43255045	5442	CGCGAGGAGGA ACAGCTCCGCCA GG/A/GJAAGGA GGAACAGCAGCT GCGCAGC	A	G	Glu	Gly (8508)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
6338	cg43255045	5801	GAGGCACCGCC AAGTCGGGGAG ATA/A/CJAATCCC AAGAAGGGAAG GGCCATGG	A	C	Lys	Gln (8509)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
6339	cg43957646	3048	GTGTTCAATTGCT GTACGTGATAAG A/GTJGCGTGAG GGGGTGGACAT GGTGAGG	G	T	Pro	His (8510)	NON- CONSER VATIVE	struct	Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa.	0	10
6340	cg42719763	755	TTCACAACCCAG CACAAACCTCTGC TTTCJCTACAACC AGCACAAACCTCT GGTCC	T	C	Ser	Pro (8511)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P98088 TRACHEOBRONCHIAL MUCIN (TBM) (MAJOR AIRWAY GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 1056 aa (fragment).	0	11 (11p15)

6341	cg42491601	1247	CAGATTCGGAGT A AACATGGAACGC C[A/C]GAACAAC GAATACCATATC CTTCTT	C	Gln	Pro (8512)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6342	cg42491601	1394	GAAGAGAGAGAT G ATAAAGAAAACC A[G/C]GAAGATTA AGACAGTCGTGC AAGAA	C	Arg	Thr (8513)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6343	cg42491601	1395	AAGAGAGAGATA G TAAAGAAAACCA G[G/C]AAGATTA GACAGTCGTGCA AGAAG	C	Arg	Ser (8514)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6344	cg43956325	1195	TGCATTTGACCT C CTCAGTCAGAAT G[C/T]TGATGAGC ATTTCTCATCA GTTCC	T	Ser	Asn (8515)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.1E-169	4 (4q21)
6345	cg43985529	972	CCATCCGAGTCC G TGGTTGAATAGG C[G/T]TTTGGCAG CTGAGAAAGTTCC TGGAG	T	Arg	Ser (8516)	NON- CONSER VATIVE	struct	Human Gene SPTREMBL-ID:Q95284 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1E-163	
6346	cg43051155	1027	TCAGCACCCATG C ACAGTGCCATTG C[C/T]CTCCTTGT CAAAGACACGCA GGCCC	T	Gly	Ser (8517)	NON- CONSER VATIVE	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 186 aa.	5.3E-103	17
6347	cg42475997	512	ACTTTAACAGGT T GGGACTTCAGG CTT[C/T]TTAGGA GGAGCCCACTGG CGCTTTC	C	Lys	Glu (8518)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q10465 TITIN, SKELETAL MUSCLE ISOFORM (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 7962 aa (fragment).	8.6E-98	

6348	cg44014373	674	TAACATGTTTTC CAAAGCAGATTT C[G/T]TGCTGTAC TGTGCCTGCAGG TCAAT	G	T	Thr	Lys (8519)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6349	cg44014373	675	AACATGTTTTC AAAGCAGATTC GT[G]GCTGTACT GTGCCTGCAGGT CAATC	T	G	Thr	Pro (8520)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6350	cg44014373	687	AAAGCAGATTC GTGCTGTACTGT G[C/T]CTGCAGG TCAATCTCCAGG GCCTGG	C	T	Ala	Thr (8521)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6351	cg43961860	1781	GTCTTCCTAGG CTTCTGTGACC CT[C]GCTTTTA GCCTCCTTCTT AATTT	T	C	Gln	Arg (8522)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q84703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	
6352	cg43918310	232	TCCAGCAGCAGC AAGCAGCCCTGC ATT[C]CCCACCCC CTCAGCTTCAGC AGCAG	T	C	Ile	Thr (8523)	NON- CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4E-50 1 (1q21)	
6353	cg43999676	535	ATTGGGTATACA GCACTCAGTGAA A[C/G]GGAGAGT CCACGTTTATTC TCCTCC	C	G	Thr	Arg (8524)	NON- CONSER VATIVE	sulfotran sferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.8E-157 2 (2q12)	
6354	cg40388639	2168	TCATCCGCTACG CTGGCTACAAGC A[G/C]CCTGACG GCTCCACCCCTGG GGGACC	G	C	Gln	His (8525)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0 (12q24.2)	12

6355	cg40388639	2170	ATCCGCTACGCT	C	G	Pro	Arg (8526)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
6356	cg40388639	4911	TATTTTGGAGT CACCTTGGGAAC GT/AJACGAAAGTG ACCAACCGCCTT AGATC	T	A	Tyr	Asn (8527)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
6357	cg43987111	1807	ACAGAGGCATAG GAGTCTGAGAAC TT/CJCGTGATT TGCCCAACAAGG GCAATA	T	C	Lys	Glu (8528)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
6358	cg43971304	1348	GCAACAGCTTT GGGACACGGCC AA/CJCGCGTG AAGGGAAGTTC GGGAGGA	A	C	Lys	Asn (8529)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6359	cg43971304	1349	CAACAGCTTTG GGACACGGCCA AA/CJGCGTGAA GGGAAAGTTG GGAGGAA	C	A	Arg	Ser (8530)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6360	cg43971304	1359	TGGACACGGC CAAACGCGTGAA GG/GJAJAAAGTTC GGGAGGAAGCT TTATGAA	G	A	Gly	Glu (8531)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6361	cg43971304	2282	GTCTGCACCTC CTCCACCAAGCG GC/JAJGCAAGC GCAACTCTGTGG ACACGGC	A	C	Ser	Arg (8532)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)



6362	cg43948262	1103	GGCTTCTTCCTT GTGCTGCTGGAT AT/C[CCCTCAGA ATCTGCTCTGTC TGCTC	T	C	Asp	Gly (8533)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa	0	21 (21q22.1 )
6363	cg43983214	594	TCCCACTCACTC ATGAGCTCAAAG T[G/T]TACAGGAC GGCGACAGAAAT TGACG	G	T	His	Asn (8534)	NON- CONSER VATIVE	synthase	Human Gene SPTREMBL-ID:Q13735 5- AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa.	0	X (Xp11.2 1)
6364	cg42721903	318	CCTAAATGACAT CACGAAAAGGGA A[G/A]AATTCTCT CCGCTGACGGC CAACCT	G	A	Glu	Lys (8535)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:Q06847 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.4E-79	

6365	cg43261057	1186	CATGTCATCAAT CCTGCCAGTGAT CJACJAGTAATAG CCATCCTGGTCC CGCTG	A	C	Leu	Trp (8536)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.1E-76	20
6366	cg43933068	534	TTAATGCGCTG AAGGTTCCCGTG CJC/TAGAGGATA AATATACTGCC AGGTG	C	T	Pro	Leu (8537)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
6367	cg43064068	1386	CTCGGAGGTAGA GAATGCACTGAT G/A/GJAGCACCC TGCTGTGGTTGA GACGGC	A	G	Lys	Glu (8538)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
6368	cg43958927	2793	GTTGATGTTCTT GTTAATTTATAG G/C/A/GTTTTTTG GGGATGTGGAG GTAGTT	C	A	Ala	Ser (8539)	NON- CONSER VATIVE	tgf	Human Gene SP TREMBL-ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	1.2E-246	
6369	cg43980446	3858	ATCTACACATTC ATTCCTGCTAG A/A/GJTATAACCA AAGGGACACTCG CAGCG	A	G	Ile	Thr (8540)	NON- CONSER VATIVE	tgf	Human Gene SP TREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1 )

6370	cg42711317	1113	TGCTGCATCTAT GGTTCTTAAAGA T[G]ATGGGATTG AAAAAAGAAGAT ATTGC	G	A	Val	Met (8541)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6371	cg42711317	1233	CCAAAAAGTGAA TATCAATGGAGG A[G/T]CTGTTTCT CTGGGACATCCA ATTGG	G	T	Ala	Ser (8542)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6372	cg42711317	1329	GCAAGGAGAATA CGGCTCTGCCAG T[A/T]TTTGAAT GGAGGAGGAGG TGCTTC	A	T	Ile	Phe (8543)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6373	cg43278427	1119	CCTTGATGTGTA ATGAGAGCAGTA T[G/C]CAGAGCTT GCGCCAGAGAA AATCTG	G	C	Met	Ile (8544)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
6374	cg43278427	1125	TGTGTAATGAGA GCAGTATGCAGA G[C/G]TTGCGCC AGAGAAAATCTG TGAATG	C	G	Ser	Arg (8545)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
6375	cg43278427	2002	TGCCCTCGTCAT CGTCTGCTGCTG T[T/C]ATGTGAAG ATCTACATCACA GTCCG	T	C	Tyr	His (8546)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)

6376	cg36988276	2239	TGCTCTTCAGCT CCCAGAGTCACC A/GA/TGGTTCCA CTTACATACTTG TCCCT	G	A	Ser	Asn (8547)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
6377	cg42899808	1092	CTGGCCACGAAC AGCAGGAAGGT GGC/TGGCCGA GCGGCGGCGTC GCAGGCGG	C	T	Ala	Thr (8548)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P34995 PROSTAGLANDIN E2 RECEPTOR, EP1 SUBTYPE (PROSTANOID EP1 RECEPTOR) (PGE RECEPTOR, EP1 SUBTYPE) - HOMO SAPIENS (HUMAN), 402 aa.	2.9E-212	19 (19p13.1)
6378	cg43306266	316	CTACACAGGCAT GTGGCGGCCCG AGC/GGTTCG CCGAGGCGCGG GGCAACCT	C	G	Arg	Gly (8549)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.8E-212	1 (1p31.2)
6379	cg43264978	153	GATGGATCTGCA CCTCTTCGACTA CTT/GCAGAGCC AGGGAACCTTCTC GGACAT	T	G	Ser	Ala (8550)	NON- CONSER VATIVE	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.4E-196	
6380	cg3001696	1341	CCCGTCCGATG GTCCCGGCGGT GGC/GC/GTGCC GCCTGACCAGG CCATCCGGC	G	C	Gly	Arg (8551)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.1E-195	1 (1p36.1)
6381	cg42704646	312	CTACACAGGCAT GTGGCGGCCCG AGC/GGTTCG CCGAGGCGCGG GGCAACCT	C	G	Arg	Gly (8552)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.1E-194	1 (1p31.2)
6382	cg2514276	645	GTACGTCACCAT CTTCTACGCCCT GGC/GCTACCA CCACATCATGAC GGCGAG	G	C	Gly	Arg (8553)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa.	7E-172	

6383	cg43040271	1300	GCITTCCTCATCT CTATCCCGCCCA T[G/C]CTGGCT GGCGCACCCCG GAAGACC	G	C	Met	Ile (8554)	NON- CONSER VATIVE	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.[pds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
6384	cg38841806	112	CAGCTGGCAGCT GGCACTGTGGG CA[C/A]CAGCCTA CCTGGCCCTGGT GCTGGT	C	A	Pro	Thr (8555)	NON- CONSER VATIVE	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.1E-67	
6385	cg1408914	623	ATCACTCATGTT AAGTTATCATCT G[A/C]TTGGTATA TGGGTCAGGGG AAGTTT	A	C	Asp	Ala (8556)	NON- CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2E-62	
6386	cg1408914	671	TTTCTCTCAGTG TTTACACAAAT G[A/T]GGTACCCA TGCTGAACCCCT TCATC	A	T	Glu	Val (8557)	NON- CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2E-62	
6387	cg43958312	1989	GACGATTGGTGA GATGGTGGCCC GA[A/C]GTAGCCT CTCCGTGGCCCT CAAGTT	A	C	Ser	Arg (8558)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15361 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 886 aa.	0	9

6388	cg43948839	1029	GCGGAAGCCTG GGGCCTGCTGC TGG[C/T]GCCCT GGGCTGCTGGG GCCGGGGCC	C	T	Ala	Thr (8559)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. pds:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17
6389	cg43328754	934	AAGACGTCGG GCATCCCCCGTT TC[C/G]GCTTCTT GTCCACGCCGTA GCTGTC	C	G	Arg	Pro (8560)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0	19
6390	cg43328754	935	AGGACGTCGGG CATCCCCCGTTT CC[G/C]CTTCTTG TCCACGCCCGTAG CTGTCA	G	C	Arg	Gly (8561)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0	19
6391	cg43962797	770	TCTACAGGATTT GCAGGGTCAAAT TTC/AJAGCTCATT TCTGCAGGTAAT AATCA	C	A	Gln	Lys (8562)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q02446 TRANSCRIPTION FACTOR SP4 (SPR- 1) - HOMO SAPIENS (HUMAN), 784 aa.	0	7 (7p15)
6392	cg44925200	651	GTGCCGGTGGT GCTCAGGGAGG GGG[G/C]ATGGG GAGAGCTGAAA TCCAGGAC	G	C	Ile	Met (8563)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q61191 TRANSCRIPTION FACTOR C1 (HCF) - MUS MUSCULUS (MOUSE), 2045 aa.	0	X

6393	cg43921342	2582	TGCTGCTCCAGC CCCAGGATGACC T[G/A]CACGGCC TGCTGCAGGATG AGCAGC	G	A	Gln	End (8564)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0	0
6394	cg43921342	2592	GCCCCAGGATG ACCTGCACGGC CTG[C/G]TGCAG GATGAGCAGCTT GGTCTGCG	C	G	Gln	His (8565)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0	0
6395	cg44130900	1153	TGATCCTATAGC TAAATGGCAA A[A/G]CTGTTAAG TACGATGTACAA GCTGT	A	G	Thr	Ala (8566)	NON- CONSER VATIVE	transcript factor	HOMO SAPIENS (HUMAN), 654 aa Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
6396	cg43011561	987	CAGACGACGAG GCCTTCGAGGAC AG[G/C]GGTGAT GGGACTTCGA GGGCCAAG	G	C	Arg	Ser (8567)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TFIIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.3E-275	19 (19p13.3 )

6397	cg44024015	1547	TGCCCTGGCTG GACACATGGCAC CTG/AJTGGGCC ACCTCCCGCCCT TCAGCCA	G	A	Val	Met (8568)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.6E-250	3
6398	cg43129605	1073	GGGATCAGCCCT GGGAAGACCCC ATC/AJCCAGGA GGTCACCTCTGA GGAGGAG	C	A	Ser	Tyr (8569)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6399	cg43129605	1100	CAGGAGGTCAC TCTGAGGAGGA GA/AJCAGGGC CACTGACTCTGC CACCATA	A	C	Asn	Thr (8570)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6400	cg43129605	1121	GAGAACAGGGC CACTGACTCTGC CA/C/AJCATAGTG TCACCACCACCA TCATCT	C	A	Thr	Asn (8571)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6401	cg43129605	400	GCCCGCGCTCG GCCGCCGCCG GTG/AJAGCGG AGCTGGACCT GGAACTGA	A	C	Lys	Gln (8572)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20



6402	cg43129605	443	GAAACTGACCAT CAGTACCTGGCC G/A/C]GAGCAGT GGCCAGCTCG GGGCAGA	A	C	Glu	Ala (8573)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6403	cg43129605	445	AACTGACCATCA GTACCTGGCCGA G/A/C]GCAGTGG GCCAGCTCGG GCAGAGG	A	C	Ser	Arg (8574)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6404	cg43257305	921	CATTCAGTTCT TGCCAGAAGGAA A[G/T]CTCGTGAT TTTCATGCCAAG CTAAA	G	T	Ala	Ser (8575)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P28347 TRANSCRIPTIONAL ENHANCER FACTOR TEF-1 (PROTEIN GT-IIC) (TRANSCRIPTION FACTOR 13) (NTEF- 1) - HOMO SAPIENS (HUMAN), 426 aa.	2.9E-228	9
6405	cg43929348	743	AAGGCCAGGGA TAAATTTCAAGA GT[T/A]GCTTTTCG GACACTTCCCTT TCTGCT	T	A	Gln	Leu (8576)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
6406	cg43929348	930	ATAAAGCACTCA TCATCTGTACTC TT[G]CTGCCGAC TGAAGGCACCCC TGCTG	T	G	Lys	Gln (8577)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2

6407	cg43051067	1324	TCAAACCTGCAC ATCCACCAAGCGA GTTA/JACACACAG GAGAGAGGCCCC TACAAG	T	A	Val	Glu (8578)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcls:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.3E-91	
6408	cg43051067	1648	TTCAGCCAGAGC TCCAACCTTCAC ATTG/JCCACACAG CGGGTTCACAAG AAAGAT	T	G	Ile	Ser (8579)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcls:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.3E-91	
6409	cg42849540	1840	CTCCAGAAAGAG CTCTGCAGGCG GA[G/C]CAAAGG CAGGGCAGCCG GAAAGCAG	G	C	Ala	Pro (8580)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcls:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	2E-88	20 (20q13)
6410	cg42532030	317	TTATAAATGTGAT GAGTGTGGGAAA [G/A]CCTTCAGTC AGAGCTCAGATC TTAT	G	A	Ala	Thr (8581)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcls:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.9E-57	

6411	cg43984952	1026	CTCGGTCCCCGT CCCTGTCCCCCA A[C/G]TCACCCCT CCCTTCTGAACA CAGAA	C	G	Asn	Lys (8582)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
6412	cg43984952	767	CCAGACGCCTTC AAGCCATCAAG A[C/G]GGAGAAG CTGGAGGAGCC GCCCGAA	C	G	Thr	Arg (8583)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
6413	cg43946772	1682	ATCTGGTCCAG TCTTTTATTTT A/CJTATCAATATT TAATATACTGGC TAC	A	C	Tyr	End (8584)	NON- CONSER VATIVE	transfe se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
6414	cg43946772	2216	TCTAATGCTGGG CACCTGGCTATC C[C/C]CTCTGTG GCTTATCCAGG CACTG	T	C	Glu	Gly (8585)	NON- CONSER VATIVE	transfe se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
6415	cg43916882	674	AAGATGAAGAGC CCCAGCATCATG G[A/G]GAAGCG CTGGCGTAGTAG GGGTAG	A	G	Ser	Pro (8586)	NON- CONSER VATIVE	transfe se	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.3E-245	1
6416	cg44017777	364	AAACTGTGAAG CAGCAGTTTGCC C[G/A]AGGATGC AGAAGGATGGCT TTTGGG	G	A	Ser	Leu (8587)	NON- CONSER VATIVE	transfe se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)- ARGININE ADP- RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	

6417	cg44017777	469	CACACCATGGTC TTCAAGCTTCTG G/A/T/T/T/T/TCTCA CCATGGTCTTCA AGCTT	A	T	Ile	Asn (8588)	NON- CONSER VATIVE	transfe se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	
6418	cg44017777	526	TTTCTCACTATG GTCTTCAAGCTT C/A/T/JGGTTTTTC TCACCAGGTTG TAGAC	A	T	Leu	Gln (8589)	NON- CONSER VATIVE	transfe se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	
6419	cg44000740	721	TGCCAGTGTCTG GGGAGATACTG GCT/C/C/CACCCA GGAAACAGGG AACATCAC	T	C	Glu	Gly (8590)	NON- CONSER VATIVE	transfe se	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.6E-117	16
6420	cg42344304	154	ATCTCACTGCAC CGCCGCCTGCC CG/A/T/JGCGCTG GAACCCGCTGTG CAAAGAG	A	T	Glu	Val (8591)	NON- CONSER VATIVE	transfe se	Human Gene Homologous to SPTREMBL-ID:O08832 POLYPEPTIDE GALNAC TRANSFERASE-T4 - MUS MUSCULUS (MOUSE), 578 aa.	1.2E-101	
6421	cg43954704	888	TCGGATATTGCC CTTCTGGATGGA G/A/G/ACTCCTTG GGGATGCTGAGT TCAGG	A	G	Phe	Ser (8592)	NON- CONSER VATIVE	transfe se	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1, O N- ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.1E-68	2

6422	cg43020771	438	ATGGACATCTGG GGGGGAGAGAA TTCTTTGAGCTC TCCTTCAAGGTG TGGATG	C	T	Ser	Phe (8593)	NON- CONSER VATIVE	transport	Human Gene Similar to SPTREMBL- ID:O08912 POLYPEPTIDE GALNAC TRANSFERASE-T1 - MUS MUSCULUS (MOUSE), 559 aa.	9.2E-51	
6423	cg38869466	218	CGGCGGAAGGT GGTGGACTGTAG CCGCGGGAGGA GACGCGGCTGT CTCGCTGC	G	C	Arg	Pro (8594)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) HOMO SAPIENS (HUMAN), 629 aa.	0	13
6424	cg43998978	4040	GGCGCCCTGGC AAATCCAGGAGA CA[G/C]CTCCGC CCAGCAGCTGG CCCCAGGT	G	C	Ala	Pro (8595)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
6425	cg43935986	1982	CTCCGGTTCTGT GAGGAACAACAT TIG/AJCTTATGGG CTGCAGAGCTGC GAAGA	G	A	Ala	Thr (8596)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
6426	cg43935986	2282	GCTGGTGATTGC TCACAGGCTGCA GJAGJCAGTTCA GCGCGCCACCC AGATCCT	A	G	Thr	Ala (8597)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
6427	cg43935986	2348	CAAGCTGCAGAA GCTTGCCAGCT CT/CJAGGAGGG ACAGGACCTCTA TTCCCG	T	C	End	Gln (8598)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)

6428	cg43112765	4285	GCTCTGATGCTT C TCTATTGTTATCC [C/T]TCCTTTTGG CGAATACCCCGC TTTG	T	Pro	Leu (8599)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:G2959643 RIM ABC TRANSPORTER HOMO SAPIENS (HUMAN), 2273 aa.	0	
6429	cg44008864	3409	CAAGGACACAGA T CACAAAGGCCTT C/T/CJCGGCGTC CAGCACATTGTT TGGGTC	C	Glu	Gly (8600)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.lpcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
6430	cg44008864	3410	AAGGACACAGAC C ACAAAGGCCTTC T/C/TJGGCGTCCA GCACATTGTTTG GGTCC	T	Glu	Lys (8601)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.lpcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	

6431	cg44008864	599	ATGAGGTTGGCT GGAGAAATCAAT TTTCJAGCTACTA CTCCTTTGTCCA GGACC	T	C	Lys	Glu (8602)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcis:SPTRMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
6432	cg43300953	244	GGCATGCGGGA CTACGACGAGGT GATTCJGCGCTTC CTGGGCGAGTG GGGGCCC	T	C	Ile	Thr (8603)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6433	cg43300953	336	CCCCAATGGCTT CAATGGTATGTC A[G/TTCGTGTTT CTGGCGGGGAC CCCCGA	G	T	Val	Phe (8604)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6434	cg43300953	414	GAACCTGAGCAGA CGCCTGGCGCA AC[A/C]ACAGTGT CCCGCTGCGGC TGCGGGA	A	C	Asn	His (8605)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6435	cg43300953	465	CGGCCGCGAGG TGCCCCACAGCT GC[A/C]GCCGCT ACCGGCTCGCC ACCATCGC	A	C	Ser	Arg (8606)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6436	cg43964039	2693	TGCAGGGTGCC CAGGGCCCCAC GAA[G/A]GGCTG TGGGTGACACTT CACCCACA	G	A	Leu	Phe (8607)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.6E-259	1

6437	cg43992017	1612	CAGCAGGAGGC CGAGAAAGACAA CG[G]ATGACCA CGCGGCGCTCC GGCGGCTG	G	A	Thr	Ile (8608)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.4E-241	
6438	cg43919987	3399	TCGTGTATGTCA CAGGCCGGCCC GA[A]TAAGAAGA AGCACCGCGTG GTGGCAT	A	T	Lys	Ile (8609)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6439	cg43919987	3401	GTGTATGTGACAA GGCCGGCCCCGA AA[A]TGAAGAAG CACCGCGTGGT GGCATGG	A	T	Arg	End (8610)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6440	cg43919987	3456	CGCAGCACAACT TCCCCACGGC GT[G]GTCCTCCT TCTGCGACGGC CTCACCC	G	C	Trp	Ser (8611)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6441	cg42876412	531	GATGCCCTCTCCT CCATACATCTA C[A]TJGCAAAGG GATCTACGACGG AGACCT	A	T	Ser	Cys (8612)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14
6442	cg43924839	1242	TCACCCAAAGAG AAGTATCTGAAC T[C]A]TTTAAAC TTTTTCAAAATAT ACTC	C	A	Lys	Asn (8613)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.6E-172	6



6443	cg43945806	600	AATCCTTCCACA GGGACGGAATG ATG/CCTGCGCA GTTCACTGTCAG CATGGGT	G	C	His	Asp (8614)	NON- CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
6444	cg43945806	601	ATCCTTCCACAG GGACGGAATGAT G/C/GTGGCAGT TCACTGTCAGCA TGGGTG	C	G	Gln	His (8615)	NON- CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
6445	cg42726186	821	ATCCAGCAGTTG GTTCACTCCAACA G/G/CJAAAATCTG AGGATCTCCTAA AATGG	G	C	Phe	Leu (8616)	NON- CONSER VATIVE	transport	Human Gene Similar to SPTREMBL- ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa.	2.5E-60	17
6446	cg43120117	1168	ATCATAATAACC GAACAACGCAGT TGTJACAGACCC AAGGTTACACCA CATCA	G	T	Leu	Phe (8617)	NON- CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
6447	cg43262192	3285	CCCACTGGCACCA AAATACTGGGCT C/A/TJCCGGTCTG GGACACATATCT GGAGA	A	T	Val	Glu (8618)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75068 KIAA0480 PROTEIN - HOMO SAPIENS (HUMAN), 1252 aa.	0	1
6448	cg43917756	889	GTCAATCATAACC ATATACTTGTTG C/G/TJGGTAGGC ATGTAACAGCCCC TGGAGC	G	T	Pro	Gln (8619)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0	1
6449	cg43929067	3507	ACCTTGCTTCTT AGATTTTTCCTTC T/A/TJTTTCTTTG ACTTAATTCCTC AAG	T	A	Lys	Met (8620)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

6450	cg43948542	1110	TGAAAAAAGGGA GCCAGTTTGGTC A[G/C]TCCTGTTG TTTGCAGCAAA AATTG	G	C	Gln	His (8621)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6451	cg43948542	1890	AAATCATATCTCT TGATGCAAAGTTI G/TJAATTTGGAA AACAAAGACTAC AAGA	G	T	Leu	Phe (8622)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6452	cg43948542	517	AAAAGGAAATGC TGCCCTGGCAAGA A[C/T]AGTTGAAA CAGAAGAAAGCT CCAGT	C	T	Gln	End (8623)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6453	cg43950151	3235	CACCTCCTCCGT AATCTGCTTAATT [A/C]GCAGCTTAT AGTCTTGAGCCA AGAG	A	C	Leu	Arg (8624)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
6454	cg43950151	4084	CTCATGGCCATC TGCGCCCTCTAC C[G/C]GCAGGAA GCAATTGGTGT GTGGCC	G	C	Pro	Arg (8625)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1

6455	cg43926985	1450	CATCATCATGGAT CCTCATCCAGTT T[G/T]CATTTAGG AGGACTGACAAA TGGA	G	T	Leu	Phe (8626)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
6456	cg43961763	1526	CTCATCGTTGAT TTGTTCAATTTT T[C]CTATATCT CTTGCTGCTC TCAC	T	C	Glu	Gly (8627)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
6457	cg43301812	3665	GGCACTGTCTTA TCCTCCTCCCTG C[A/T]GACCTCTG GGTTGCGTCTT TCTCC	A	T	Cys	Ser (8628)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
6458	cg43301812	3980	TGACCCCTCAGCT TCAGCTGCAAAAT TT[C]AGAGTTTG TGGAGTTATGAG AACTA	T	C	Lys	Glu (8629)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
6459	cg43925942	2191	GGTTGCTTGGGA GACCCCTACAAGA A[A/G]AATTTTCC CGCTTTATGACA GAACC	A	G	Lys	Glu (8630)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
6460	cg43931104	825	GTGTGTTTCATG TGGACATTGTTC ATT[C]GGCTGGC ACTTTGGCAACC TTTGTG	T	C	Met	Val (8631)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa.	0	3
6461	cg43939697	314	GGCCGCTCAAA GCCGGGAGATC GAC[G/T]GTTTGA GCCCGGAAGCG CAGAAGCT	G	T	Gly	Cys (8632)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3

6462	cg43940975	315	TCTGGATCCACG GAGAAATATCCA A[G/A]ACGCTCAA ACTGGAACCTTGT CGAAG	G	A	Leu	Phe (8633)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
6463	cg43917191	3407	TCCTTTAATACT GAAGTTGTATCC T[C/A]AGGCAGC CGGCTGTTAGCA TTATCT	C	A	Glu	End (8634)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
6464	cg43934651	1011	AGGATTTTGATA ATTCTCATAATA [G/C]AATCCAGTA TCTTGATATCAG TGTT	G	C	Arg	Thr (8635)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa.	0	4
6465	cg43934651	2577	GCTGTGACTGTG ACCTCCCTCTGC A[G/T]CTACTTGG ATCTGCCCTGGT ATCTC	G	T	Ser	Ile (8636)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa.	0	4
6466	cg44035533	1188	GAGAGCGACAG CCCAGATAGCCA CTT[C/G]GGACCTG GAATCCAACGTG GAGAGT	T	C	Leu	Ser (8637)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78316 HYPOTHETICAL 99.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 873 aa (fragment).	0	4
6467	cg43933355	1258	GTTC TTGAACA TTCCTCCATCCG G[A/T]CATGGAAG GGTCGCAAGTTA TCTGA	A	T	Val	Asp (8638)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
6468	cg44026925	3702	CCCTGTGTGCTC TAGGGTTGGCAA TT[G/C]CAGGATGC TACACTGTCAAA AGCAG	T	G	Ile	Met (8639)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5

6469	cg43924112	4800	GGTTTAAAGGAT TGAAGAAATTCAC G[C/A]GTGAAGG GGAAAGTGTTCC AAAGGC	C	A	Arg	Leu (8640)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
6470	cg43975893	517	CTTTGGTGAGC TTCAGTATTCTC A[C/A]AAGAATCT TGGGTAGGTTTC TTGGT	C	A	Cys	Phe (8641)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45157 FLASH - HOMO SAPIENS (HUMAN), 1269 aa (fragment).	0	6
6471	cg43918128	2125	TCATCAAGGGCT CCGTCCTCTCCC TT[C]CTCGCCGC CTTCGTCATCAT CCTCA	T	C	Lys	Glu (8642)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14137 HYPOTHETICAL PROTEIN KIAA0124 - Homo sapiens (Human), 682 aa (fragment).	0	8
6472	cg43968274	1803	AATGACTGAAGT GGACCTCTTCAT T[C/T]TACCCAG AGAATCAAAGTG CTGAA	C	T	Leu	Phe (8643)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
6473	cg43968274	1804	ATGACTGAAGTG GACCTCTTCATT C[T/C]TACCCAGA GAATCAAAGTGC TGAAC	T	C	Leu	Pro (8644)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
6474	cg43287069	2139	ATACTCTATCTG GATCTTCTCTCA G[A/T]CAGGCAC CATCTCATATGT ATGGCA	A	T	Arg	Ser (8645)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa.	0	11
6475	cg43925880	1137	TCTTCTCAGTC TTGGTCTGAAAT T[T/C]AGCAGCAT TGGTCCAAACA CGTCC	T	C	Lys	Glu (8646)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13435 SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa.	0	11

6476	cg43916884	2403	GATCCCTTTTGG TAGCTTTCCAGG C[A/G]ATGTTTG GCCTCAGGAGA CTTATT	A	G	Leu	Ser (8647)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6477	cg43916884	340	GCAGCTTTCTCA AAAGGCTGCTCT G[G/C]CAACTGC TGCTTCTCAACC CCCTTG	G	C	Pro	Ala (8648)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6478	cg43916884	341	CAGCTTTCTCAA AAGGCTGCTCTG G[C/G]AACTGCT GCTTCTCAACCC CCTTGG	C	G	Leu	Phe (8649)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6479	cg43924701	1114	AGAACTCGGCA CTGTTTCGTAGG A[A/T]CGCGTGAA GTTTCAGGAAC AGTCC	A	T	Phe	Ile (8650)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
6480	cg43929104	2468	TGGTGGCCATAG AGGACGTGGAG GAT[C/T]CAATAT GCGTGGTGGAA ATTTCAG	T	C	Phe	Leu (8651)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
6481	cg44018598	4168	GCAGGATACCAT TCAGTCTCTCTCC G[C/T]TGCAGACA CCACACTTACAA CTTTT	C	T	Ala	Thr (8652)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
6482	cg43936094	1825	ACTCGGGGCAC GACACGCGTGAA GG[G/A]TTTATCA TCTGGTGACAAG TTAGGT	G	A	Pro	Ser (8653)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa.	0	15

6483	cg43928515	508	GCATTTTCTACA CTTGTTGTGAAC AT/CJGTGGCTCA GGGAAAGGGGT AGGATC	T	C	Met	Val (8654)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
6484	cg43945577	2253	GTTGACAAGCCG GCTACAGGGAGT C[G/C]GCGCGCT CGGCCAGGCAG CCTCTGA	G	C	Gly	Arg (8655)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
6485	cg43945577	408	GGAGGTGGAAG TGCTGGAGGATG AC[G/A]TGTCTGC AGTTGAGTTCAG GCAGAC	G	A	Val	Met (8656)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
6486	cg43964911	2441	AAGCAGAACAGG CACAGGATGTAG G[G/T]GGTAGTC AGGAGTGCGG CAGCTGG	G	T	Pro	Thr (8657)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
6487	cg43983241	1570	ACCAACGACAG TTTAAAGTTTAC [C/A]AGAATATCT TGAAAATATGGT AATA	C	A	Pro	Gln (8658)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0	18
6488	cg43983241	402	TACTTGGAAATC AAATACATTCTAT [T/G]CTGCTGGG AAAAATTACTTAC TACG	T	G	Ser	Ala (8659)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0	18
6489	cg43991657	2076	CCAGGCCCTCCT CAGGCGGCTCC AGG[C/T]GCGGC TGAGGAGGCCCC ATCACTGGG	C	T	Ala	Thr (8660)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19

6490	cg43919691	1205	CTTTCCAGCTC TGCCTCCAAATG C/A/G/ACGTGTG CTCCCTCACCTG GTCCGA	A	G	Leu	Ser (8661)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
6491	cg43919691	830	GAGCTTCTCCAA TTCTTCTTGTAAAC [C/A]GACATGCC GAGGTCTGAGC CTCCTC	C	A	Arg	Leu (8662)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
6492	cg43949984	1626	AGGAACACCCAC AACATCTTCCAA A[A/G]TCTTAGTA GGGCAAGGTCT GGAATG	A	G	Ile	Thr (8663)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76931 FLS353 - HOMO SAPIENS (HUMAN), 747 aa.	0	20
6493	cg43981483	439	GGCAGCCCGAGG TGATGTTGAGGT TG[G/A]AATTCTT GGAGGCATTGAT GAACAT	G	A	Ser	Phe (8664)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa.	0	20
6494	cg43955358	2797	TTTTCTGCAATCT CCAAAGCTTTCC[ A/C]TGCTTTTCT GTAGTAAAGAGC TCA	A	C	Trp	Gly (8665)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
6495	cg17663981	361	GGCCGCCACCC GGAAGGCCGCC TGC[A/G]CCTGC GACCAAAAACCC TGCAGCTG	A	G	Thr	Ala (8666)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)



6496	cg17663981	388	CTGCGACCAAAA ACCCTGCAGCTG C[C/T]CCAAAGG GGATGTCAACTA CGCGTT	C	T	Pro	Ser (8667)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)
6497	cg43968854	9932	GACAATGTGTGT GTCAAGAAAATA A[G/C]AACCCAGAA GTCATAGGGACA GTGAA	G	C	Arg	Thr (8668)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6498	cg43968854	5060	GCCTGCAAAATCT TCACAACCAGAC C[C/T]AGACAAAA ACCCAGCAAGCT CCAAG	C	T	Pro	Leu (8669)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6499	cg43968854	8018	ACAAAGAGATGC CCCAAGACACGT C[C/T]CAGGAAA GAAGTAAAGAG GAGCTC	C	T	Pro	Leu (8670)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6500	cg43269831	1626	GTGGCGATCATC ATGAAAGAGGGC T[C/A]AAAGTTGG ACTTGTAGTCCA GAAAG	C	A	Glu	End (8671)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15586 N-ACETYLGLUCOSAMINE-6- SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6- SULFATASE) - Homo sapiens (Human), 552 aa.	0	12 (12q14)
6501	cg44920831	1083	CTAGAAAGGGGTA ACAGCTCTGTTC G[C/A]TGCAGGA CTAGCAGGCGTA GGAGAT	C	A	Ala	Ser (8672)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99493 SCA2 PROTEIN - HOMO SAPIENS (HUMAN), 914 aa (fragment).	0	12 (12q24)

6502	cg43979900	2115	GGTCTCTATGTA AACATCACAATT TTAGTAGTCAGA TTGGTCCAGTTG TAGTC	A	G	Ile	Thr (8673)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3 )
6503	cg43979900	2601	AAATTGTTGTGA CACATTGAAATA A[G/A]GAAGAAAT GGCCGTATGCAC TTAGA	G	A	Pro	Leu (8674)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3 )
6504	cg43960198	1948	GAACACGATCTG GTTCAATGTGACC A[G/T]GAAGAACC ACGCCAGGCAG GCGGGA	G	T	Arg	Met (8675)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
6505	cg43960198	1978	AACCACGCCAG GCAGGCGGGAG TTC[G/T]AGGTCT TGGACATCAAAG CTGAGTC	G	T	Arg	Leu (8676)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
6506	cg43973129	1847	CAACTATGACTG GTGGGAGAAAAA G[C/G]CCTTCTCT GAGGATGTGAAC TGGGG	C	G	Pro	Ala (8677)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETORIN I PRECURSOR (SGI) (CHROMOGRAININ B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)

6507	cg43973129	657	GGAGAGAACTAT CAAAAAGGGA GC/A/GJAGGGA AGATAGCAGTGA AGAGAAA	A	G	Gln	Arg (8678)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETAGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)
6508	cg43955813	1322	CTGGATACAAGT TATGCTTTGATA G[G/A]TGAAACA GTAAATAATTATA GATCT	G	A	Gly	Asp (8679)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
6509	cg43955813	691	ACAAAATGTTATT CCATCTAGTGCC [A/C]AAAAAGAGAG AGACTTACACTT TTGA	A	C	Lys	Gln (8680)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
6510	cg25268354	1654	CTCTGTTCCCTG GAACTCCTTCAA C[C/T]GCGACGT ACTGAAGGCCCT GTACAG	C	T	Arg	Cys (8681)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa.	0	9 (9q34)
6511	cg43311566	794	AAGAGCGAGTG GGCCAGCGAG CGA[A/G]CCCTG AGGACCTGGAAT TCATCCGC	A	G	Asn	Ser (8682)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
6512	cg43992229	1269	CCAGCCAGACTG TGACTATGTTGT G[G/A]AATTGCAA GCCATAACGTAC TGGGG	G	A	Glu	Lys (8683)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
6513	cg43992229	1770	CAAGCCTATTGG CTGCCTGGCG AA[C/G]GAGGTC ATGTTCTTCTAA GGTGCT	C	G	Arg	Gly (8684)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)

6514	cg43992229	1771	AAGCCTATTGGC TGCCTGGGCGA AC[G/C]AGGTCAT GTTCTTTCTAAG GTGCTA	G	C	Arg	Pro (8685)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
6515	cg42681986	1609	GCCAGTGGTGG CGGGGAAGAGA ATT[C/T]GCGACA CAGACGTGGGG ATTGGCCA	C	T	Glu	Lys (8686)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14827 RAS-GRF2 - HOMO SAPIENS (HUMAN), 1237 aa (fragment).	0	
6516	cg42682094	3090	GACTGCTGTGAG GACAGGGCTGG CG[C/T]AGAGCG AGCAGTCACAGG TGGGTGA	C	T	Cys	Tyr (8687)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
6517	cg43054046	717	TTTTAAGTGA GTTCAAGAGTTT TTT/AAGAATGT GGCAGTGATCCC TCCTG	T	A	Phe	Leu (8688)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa.	0	
6518	cg43139712	1735	TAAGACCAGGGA AAGGGGGAGC AG[G/C]GGACAA AGAGGGGCCCG GGCAAGCA	G	C	Gly	Arg (8689)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	
6519	cg43139712	1745	GAAAGGGGGGA GCAGGGGACAA AGA[G/T]GGGCC GGGGCAAGCAC TTCATCGGA	G	T	Arg	Met (8690)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	

6520	cg43920875	2051	CCTATACTGAGA TAAAGCAGCCCC A/G/TJTGACACA TCTGTTGGCCAG GGCCA	G	T	Thr	Asn (8691)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
6521	cg43932090	251	GACTTTAAGGCC TTGTCTTTACCTT [C/T]ATCCTTTAT GAAGGAAGCTTT GCCA	C	T	Glu	Lys (8692)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
6522	cg43934688	1393	GGTTCAGTTAAA CCTACTCAAACCT A/A/TJTGCTGTTA AAGAAATCATTGA CTACA	A	T	Asn	Ile (8693)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
6523	cg43992835	1306	TTCATCATTGTC CGAGTCCACAAC C/A/CJCTGCACCTG ATACCGTCCGCT ACAGT	A	C	His	Pro (8694)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60292 KIAA0545 PROTEIN - HOMO SAPIENS (HUMAN), 1129 aa (fragment).	0	
6524	cg44016445	1774	TCCTCCCCGGG GACATGGCTGTC GA/A/TJGAAGTCA ATCTGCACAGGG TCCCCG	A	T	Phe	Ile (8695)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa.	0	
6525	cg44024279	1391	TGAATGCCAAGA TAAAGGAGAAGA A/G/TJAATTACAG AAATACATCCAG GAGAG	G	T	Glu	End (8696)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
6526	cg44130923	2147	CCAGTTTCTCAA GATATGCCTGGC T/A/GJAAGACGAA GGGCTCCTCACC ACTGA	A	G	Lys	Glu (8697)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa.	0	

6527	cg43957199	801	CCCATGAGGTTG GGGGTGAAGTCG ACTTCGATGTCA ATGGTCAAGATG TCCCGG	T	C	Ser	Gly (8698)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
6528	cg43978095	1436	GTGCCTCTTCAC CAAGAAATGCTGC A[G]TCGGAGCA CGCAGACCACAA ACGACG	G	T	Gln	His (8699)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15326 BS69 PROTEIN - HOMO SAPIENS (HUMAN), 562 aa.	2.0e-317	10
6529	cg43937128	2000	GTTTCTGGCACC CACTTGAGTCCG G[A]GCTGCAGT CTCTGGAAGAAG GAGCGG	A	G	Ser	Pto (8700)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
6530	cg43956210	1439	CCCTGTAATCCT TTCTGCTCCTTG G[T/A]ACTTAGAT TTGATTAGCTAT GGACA	T	A	Tyr	Asn (8701)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
6531	cg43956210	1477	TTAGCTATGGAC AAGATTGGAGGA A[A/C]TACTATAA AGTGGAACCTCT TGATT	A	C	Lys	Asn (8702)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
6532	cg43254411	1198	TGTGGGATTTT CAGAGGACAGT GC[T/C]GACGTG CATACCATCTT GAGAATA	T	C	Gln	Arg (8703)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35610 STEROL O-ACYLTRANSFERASE (EC 2.3.1.26) (CHOLESTEROL ACYLTRANSFERASE) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) - Homo sapiens (Human), 550 aa.	5E-305	1 (1q25)

6533	cg43917155	256	AGTGACATTTGG AAGCTTTTCAAA C[G/A]TGGTTCCC TG TAGTCATCCA TATAT	G	A	Val	Met (8704)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
6534	cg43998124	2794	TCGCACAGGTCT CCATTCCTCTCC T[A/C]TGCATTAC ACGTGCTCTAA GACCT	A	C	His	Gln (8705)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	
6535	cg40918088	1870	ATTAAACCTCTG GATGTCGCCACG ATT[A/C]GCTCTCCA GTGCAAAAGCCA CAGAG	T	A	Ile	Asn (8706)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
6536	cg43931056	975	AAGCACTACAGC AGCTGGAGAAAT A[A/T]AAACCCTA TGAAGAAGCACT GTTGC	A	T	End	Tyr (8707)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
6537	cg42709686	1613	CATCTCTGACTG GCTGCCAACACT C[A/G]TGAAGCT GGCCAGGGGAC ACACCAA	A	G	Met	Val (8708)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYLGALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
6538	cg42709686	1667	CACAAAGCCTCT GGATGGCTTCGA C[G/A]TGTGGAA ACCATCAGTGAA GGAAG	G	A	Val	Met (8709)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYLGALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
6539	cg43949830	1097	ACTTTTCTGGA TTCACCATTCAG A[C/G]AATGTTTC AGGCTGGCACTC TTACA	C	G	Cys	Ser (8710)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16

6540	cg43949830	1106	GGATTACACATT CAGACAATGTTT CJAGJGGCTGGC ACTCTTACACCC AGCACT	A	G	Leu	Pro (8711)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
6541	cg43949830	852	AACAATCTAATT GCTCGGTACATT C/TGACAAATTTT CCAGACTCAAAG CTG	C	T	Glu	Lys (8712)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
6542	cg44910613	515	AGCACCTCCTGT TATTCCAAATGT G/C/GJCTTTCCTC TGGGCCTGGAAT GCCCC	C	G	Pro	Ala (8713)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P38567 HYALURONIDASE PRECURSOR (EC 3.2.1.35) (SPERM SURFACE PROTEIN PH-20) (SPERM ADHESION MOLECULE 1) - Homo sapiens (Human), 509 aa.	1.2E-280	7
6543	cg43963979	1906	AGGAGGCGTTTG TCTTGGTAGCGC C/G/AJCAGAGCA GACAGACGCTG CTGGCGA	G	A	Arg	Tyr (8714)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
6544	cg43333012	1030	CCATACCTGTCA TCTGAGATCCTA A/G/AJCATGATCA TGCCATGCAACT CCATA	G	A	Leu	Phe (8715)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272 (11q23.3 )	11
6545	cg43333012	1864	AATAAGCCCTCA ATCCGAGTTCGG GT/GJCATTTCGA CAAAGTGTGCGAG AAAGA	T	G	Thr	Pro (8716)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272 (11q23.3 )	11
6546	cg43958878	1321	TGGTGGGCGTC TGGCTGTTTCA G/G/AJCTGGTTCT CCTTGCTCAGGA GGAAG	G	A	Pro	Ser (8717)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9



6547	cg43313186	417	CCGCGTGACGG TGCGCAAGGCC GAC/A/GJCCGT GGCTGGGCAT CAGCATCAA	A	G	Thr	Ala (8718)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
6548	cg43056973	691	AAGTGCCAGTGA AGCCACCCCTGGT G/GCJCCCTGCT GGCCGCTCGGA CCAAAGT	G	C	Ala	Pro (8719)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa.	5.2E-262	7 (7p11)
6549	cg43980777	1015	CATGGGCTCTGG TACAATCTGGGG T/C/GJGTGAGCA AGTGGCTTCTTG GCCCTC	C	G	Arg	Pro (8720)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
6550	cg43980777	1016	ATGGGCTCTGGT ACAATCTGGGT C/GCJTGAGCAA GTGGCTTCTTG CCCTCC	G	C	Arg	Gly (8721)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
6551	cg39711096	943	GTGGAGGTGGA CATGTCGGGAGA CTT/CJGGGGTG GCTGTTGAACCT CTCCAC	T	C	Leu	Ser (8722)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1E-251	
6552	cg42101957	375	CATGAGATCCAT GTTGGTGTCTGC C/T/GJTTTGTC ATGACTGAGTAG GTCTT	T	G	Lys	Asn (8723)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA- INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa.	5.5E-251	20 (20q12)
6553	cg44910581	2259	CTTGAGCCATCT AGCTTCTCACCA C/T/CJGCAATACC GGTTGGGTACTG TGCCA	T	C	Cys	Arg (8724)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	

6554	cg44910581	2780	GGTTAGATAGCT CTTTATTGTCAC G/A/GJATTTGGTG AAAAATACTTAG GGATG	A	G	Glu	Gly (8725)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	
6555	cg43995664	1356	CAGAGGCCGCG AGGACGCAGTG CCC[G/C]CCCCA GCTGGAGGGTG CCTGCCATC	G	C	Arg	Gly (8726)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
6556	cg43985612	708	TTGATAGATCTT GATTCCAAAATG CT/AJCAATCTCC TCCCGGATTTTG CGTTT	T	A	Glu	Val (8727)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa.	6.9E-244	17
6557	cg44021361	332	CCAGCACCAAC AACCTGAGCAGG TG/TJTGAGCC AGCGTGCAGGC ATGGCC	G	T	His	Asn (8728)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
6558	cg44021361	334	CAGCACCAACAA CCTGAGCAGGT GT[G/T]TGAGCCA GCGTGCAGGCA TGGCCCA	G	T	Thr	Lys (8729)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
6559	cg43950654	111	TCCCTTTCTTG GGCAAGATGGC GG[C/A]GTACGA CTTGACTACTCG CATCGCG	C	A	Ala	Glu (8730)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
6560	cg43950654	202	TTCTCTCTGTAA AGGAGATATATA ATT/AJGAAAAGGA ATTATTACAAGG TAAAT	T	A	Asn	Lys (8731)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6

6561	cg42750618	359	ATGCGCATGAAT GCGGGCCAGCC TG[G/C]GTCAGT GGGGCTGAAAG GGCAGAGG	G	C	Pro	Ala (8732)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	2.9E-238	1
6562	cg43922856	1184	TTTCCATAGCTT GATAGACCAAAA A[C/A]AAAAAAC TGCCACAACAAC AAACA	C	A	Leu	Phe (8733)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42167 THYMOPOLYMER BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2E-237	12 (12q22)
6563	cg44013460	1021	ACTGAGTTGAAA AAGCTGGACTTC C[C/G]AGCTCCA ATTGGACCCAGC AGCAGA	C	G	Gly	Arg (8734)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
6564	cg44013460	621	CACACCAGCGTT TACCAACTCCCT T[C/T]GAATCTT TTGATCTTTACTA TCAT	C	T	Arg	Gln (8735)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
6565	cg41027023	815	AGCAAGAGACAA CTGCAACTGGG GGT[A/G]GTCAC CCTGGACAGCA GCTCTGTT	T	A	His	Leu (8736)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P24278 ZINC FINGER PROTEIN 48 (ZINC FINGER PROTEIN KUP) - Homo sapiens (Human), 433 aa.	3.5E-233	
6566	cg43968343	2741	CTGAATAGGAAG TGTCATGAGGTC T[C/T]GGTCCAAG AAGAGTCTCAGA AGGAA	C	T	Arg	Gln (8737)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231 (18q21.3)	18
6567	cg43916785	3089	TCCATGGGTCT TCTCGTTTTCTT [T/C]TTTTCTTG CTTTCTCTCTCC TCC	T	C	Lys	Glu (8738)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14

6568	cg43916785	3425	GCCATTCTCTT CTCTTTCTCTT [C/T]CTTTTCAGC TTCTTTCTCATAT TCC	C	T	Glu (8739)	Lys (8739)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
6569	cg43916785	3431	TCCTCTCTCTTT CTCTCTCTCTTT C/TJAGCTTCTTTC TCATATTCCTGG GTT	C	T	Glu (8740)	Lys (8740)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
6570	cg43918854	1087	CAGTTCTCTCATG ACTTCCCCCATG C/G/CJTGGGCA GAACTGGGAACA GCATGT	G	C	Arg (8741)	Pro (8741)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
6571	cg43918854	1438	TTACACATATGAA ACACAGGCCTCC TT/C]GTCAGGCC CCTACTTAACCT CCGTG	T	C	Leu (8742)	Ser (8742)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
6572	cg43929685	303	CACCAGCTCACT GAGGAGCTTTGT C/T/C]TCTCTGGA TCAAGAGTCCCA CCTGA	T	C	Arg (8743)	Gly (8743)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) (2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.4E-225	12
6573	cg43929685	444	CCTGTGGGGTG GATGCTGCCTGG AGT/C]GTGCTG GGTCTATGAGAG AAATGAG	T	C	Thr (8744)	Ala (8744)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) (2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.4E-225	12
6574	cg43918561	1232	GAAATTGAGAAG CTGTCCACGCTG T/A/C]CTGGTTCA CGGTGGAGTTC GGGCTG	A	C	Tyr (8745)	Ser (8745)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)

6575	cg43918561	1233	AAATTGAGAAGC TGTCACACGCTGT A/C/A/TGGTTCAC GGTGGAGTTCC GGCTGT	C	A	Tyr	End (8746)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)
6576	cg43062448	1351	ACAACCTTAAAG GAATCCATAAAA T/G/T/GTGAAGTC CCAGGAGCTCCA CAAAAT	G	T	His	Asn (8747)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
6577	cg44021565	1014	CCTCAAGGCCAG AGGTTCTCCTTC C/G/A/TGAAGACT CTGCTGGAGACC TGCAG	G	A	Thr	Met (8748)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6578	cg44021565	345	ATGTCTGTCTTC TTGAAGGCTGGA A/A/G/TTACCTTC TTCTCATGACCA GAATC	A	G	Ile	Thr (8749)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6579	cg44021565	507	ATGAAACCAGAC AGGAGTTGGTAA C/T/C/JGGAGGCC AAGCACTTGAAG CTCCAA	T	C	Gln	Arg (8750)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6580	cg43959472	1586	TTGAGCCACACG ATGCCGCAGGTA C/G/A/CGTGAAG GGGTTCTCGTTG ATCTGC	G	A	Arg	Cys (8751)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
6581	cg44128902	1009	CAGGTGGAGTCT GTACAGCTCAAA G/T/A/CAACATAG CCCGAAAACAGC CCATG	T	A	Val	Asp (8752)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)

6582	cg44128902	1068	CGCTACTGGCAA GTCTGTCTGGGG CT[G]CCCTCGCT GTCCAGAACAGC CCTAA	T	G	Ser	Ala (8753)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
6583	cg44128902	81	CGAGGAAGAGG AGGCTCTGCAGA AG[G/A]AATTCAA CAAGCTCAAGAA AAAGAA	G	A	Glu	Lys (8754)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
6584	cg43973314	598	ACTGTTTAAACA GGAAATGGTGAC T[A/G]TTACAGTA GTGGGAATGATC TGACT	A	G	Tyr	Cys (8755)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
6585	cg43988090	964	ATTCCTACACCT GCGTATCAGTCC T[C/T]ACCAGCAG GAGGACATGCAC CAACT	C	T	Ser	Leu (8756)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88695 ALIX - MUS MUSCULUS (MOUSE), 869 aa.	5.8E-192	3
6586	cg43968431	442	GCCTTGATACATC TTCTTCATGGCC TT[G]GGGAGCC AGGAACTGAGAA GATTTA	T	G	Lys	Gln (8757)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
6587	cg43968431	547	ATGACGCAGCTC TTGGGCCCTGTG C[T/C]CTGGATGA GGTAGCCCGTCT GGATG	T	C	Ser	Gly (8758)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
6588	cg43939832	1182	GTCTTCACTCCT GATGGAACCTGC A[G/A]CAGAGAG GCTTCGACGTG TACCTT	G	A	Ser	Asn (8759)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA06754 JM5 PROTEIN - HOMO SAPIENS (HUMAN), 360 aa.	1E-191	

6589	cg43933608	378	CCGAGACCAAT CCTTGAGTTCA G[G/C]AGGGCT GTAAGGTGAAGA AGCATG	G	C	Arg	Ser (8760)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6589	cg43933608	380	GAGACCAATCC TTGAGTTTCAGG A[G/C]GGGCTGT AAGGTGAAGAAG CATGAA	G	C	Arg	Thr (8761)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6591	cg43933608	386	AAATCCTTGAGT TTCAGGAGGG CT[G/C]TAAGGTG AAGAAGCATGAA ACTCAG	G	C	Cys	Ser (8762)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6592	cg43957632	1221	GGCCACCGCGG CGGCGGCGCA ACC[G/C]GCGGG GGCCCGCAGGC GGCCAGGCG	G	C	Pro	Arg (8763)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6593	cg43957632	433	GCGGTCTACTGC ATCCGCTGGGTG T[G/C]CACCCCG CGAGCCTCCTGC TGCTCA	G	C	His	Asp (8764)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6594	cg43957632	442	TGCATCCGCTGG GTGTGCACCCC GC[G/A]AGCCTC CTGCTGCTCATT GTAGAA	G	A	Arg	Cys (8765)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6595	cg44128927	838	GGGGCTGCCCG AGTGCACGCGCT GC[G/T]GCCACG GCATCGTGGGC ACCATCGT	G	T	Gly	Cys (8766)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5

6596	cg43249165	770	GGAAGTCCTTGT TCCTGAAGCCTC A/A/G/AATTGAT GAGTGGGAGCC TGAAGG	A	G	Lys	Glu (8767)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	7.5E-183	
6597	cg42733081	806	CTGAGGTGTGG GCCTCCCTGGG ACC/A/TCCGGTC CAGGCTGTTGCC CCGGTGA	A	T	Trp	Arg (8768)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75791 GADS PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	1.8E-181	22
6598	cg43918452	391	TAGCCAGTCTC TCCGACCTTCCC TT/C/CACGCGTG CCCAGTGACTGG CCTCA	T	C	Phe	Ser (8769)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83027 KIAA1075 PROTEIN - HOMO SAPIENS (HUMAN), 1400 aa (fragment).	3E-179	12
6599	cg44035161	712	CAATGCTGGAGC AGAAAGGATCAC A/G/C/ATGTGGCT TTGGATTTCTGG AGGAG	G	C	Asp	His (8770)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14656 TORSINA - HOMO SAPIENS (HUMAN), 332 aa.	2.1E-178	9
6600	cg43933591	3997	CTGAGATAAAAT TGTGACACCAAT G/C/A/TGCAGTAT TCAACACTATCC TGTA	C	A	Ser	Ile (8771)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
6601	cg43285900	288	AAATATGATCCA AGGAAACTACGG A/C/TTCCTTCCT GAACCTGCCCTGCT GTTGG	C	T	Leu	Phe (8772)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34058 CGI-63 PROTEIN - HOMO SAPIENS (HUMAN), 373 aa.	4.1E-175	1
6602	cg43941890	1343	AGGCTGGGCTT GGGACCTTGTC T/C/TCCCAGTTG GCCTACTGTTAC ACATT	C	T	Pro	Ser (8773)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	



6603	cg43918085	1492	AAGGCTTTTGCT TCACCTTGAGTGT TTC/AJACATGTT CACGCTCTCTCTG GAGCT	C	A	Glu	End (8774)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
6604	cg43926685	355	ATGCGCATGACA GTGGCTGACGG CA/CJTGTATAC ATAGCCCAGCAG ATGCAC	C	T	Thr	Ile (8775)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	1 (1p36.33)
6605	cg43926685	491	TTCACTACAATT CTAAATACAAGA G/C/GJTATGATAT AGCCCAAGATGC GCCGG	C	G	Ser	Arg (8776)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	1 (1p36.33)
6606	cg43926685	857	ATTACCGCAGGA CCCAGCCCTGA A/C/AJACAGAGT GGTGAATCCAA CTTCC	C	A	Asn	Lys (8777)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	1 (1p36.33)
6607	cg43959938	1723	TGTTGCACCTCA CGCAATGCTTGG C/A/CJAACCTTGGT CTCATGGCAAGT CACGC	A	C	Phe	Leu (8778)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.2E-168	X
6608	cg42477985	863	ATGACACTGAGT CCAGATCTTCAC ATT/CJAGGCAT GGGTCGATTCTC GCCTGC	T	C	Met	Thr (8779)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	3.6E-167	17
6609	cg43996522	383	GTCATAGTATGT AGGAAGATTCTGA A/G/JAGAAAAAC TGCACCTTCACA TCATC	G	T	Ser	Tyr (8780)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	3.3E-166	

6610	cg44003630	966	GGAAAGTCCAG GCGGGGCTTGT GGT/CJGGCCGT GTACCACAGGAA GATGCTG	T	C	Thr	Ala (8781)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
6611	cg44003630	1613	GAGTGCCGAC AGCCAAGACGTA CT/GJGGAGGA GAAAGCGCCG CGTGAGCC	G	T	Gln	Lys (8782)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
6612	cg42712022	386	CGCTTTGACCA GAGAGGAAAGC GA/GJAATTGA AAGATATGGTGG GAATGA	A	G	Lys	Glu (8783)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
6613	cg43986534	768	TTCTGCTACGAA TTCCCCCTCCCG C[G/C]GGTGGCC ACCACCCACCCG CCCCCC	G	C	Arg	Pro (8784)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP2/22A - HOMO SAPIENS (HUMAN), 390 aa.	4.7E-160	
6614	cg43055617	1416	CCTGAGGCTGTGA TACCAGCTCCCA G[A/C]GTGACTG GCTTCTCAGCAG ACCACT	A	C	Ser	Ala (8785)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27736 CGI-27 PROTEIN - HOMO SAPIENS (HUMAN), 297 aa.	3.7E-158	21
6615	cg43287561	745	CATAGGCCCCAC TTTCAGTTGAGG A/T/GJAATCTGCC AGCATCACGTGC CTCTC	T	G	Leu	Phe (8786)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)
6616	cg43287561	799	CAGGGTCCACCA TGGTCCGAGGC ATT/CJATGTACA GCTCCTTGAAT GGTCAA	T	C	Ile	Met (8787)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)

6617	cg41629243	582	CTCCCATGCTT GAAGTGCTCTGC C[C/T]CCTTCACG CGCCACAGCATC TCCAG	C	T	Gly	Glu (8788)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	7.8E-155	19 (19p13.3)
6618	cg43992304	588	CAGCTGTCAGCA AAATCGCCATCT G[A/G]AGATCATA GAGATGGAGTG GGACTG	A	G	Phe	Ser (8789)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92503 SEC14-LIKE PROTEIN - Homo sapiens (Human), 715 aa.	1.1E-151	17 (17q25.1)
6619	cg42712956	357	TGTCATCCGACA GCTGGCAGCC TG[A/G]GTAAATA TGCAGAGGACAT TTTTGG	A	G	Ser	Gly (8790)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA81795 WASP-FAMILY PROTEIN - HOMO SAPIENS (HUMAN), 498 aa.	3.1E-151	
6620	cg42197063	739	GGCGCCATTGC CCTCAGCCTCGT GG[A/C]CATGGG GAGTCTGATGG GGAACG	A	C	Asp	Ala (8791)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75631 UROPLAKIN III - HOMO SAPIENS (HUMAN), 287 aa.	3.3E-150	
6621	cg43919239	396	ACCAGCATTAC ATGCATGGCTGC A[G/T]CATAGAAC CTCGCCACTTCC TCGTT	G	T	Ala	Asp (8792)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
6622	cg43919239	645	GTTGCTCTTGCA CGTGTGGGAGG TG[T/A]GACAATC CTCCCACACGCG CTGACA	T	A	His	Leu (8793)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

6623	cg44921374	2813	GTGAAATCTGG ATATAAACTGG T[AG]GTCCTGAG GATAACGGAATG AGGCA	A	G	Tyr	His (8794)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
6624	cg44921374	3118	TGTAAGATCTTG TGCCACTGCTAA C[G/A]AGCCTCT GGGGCCGCCTC GGAACAA	G	A	Ser	Leu (8795)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
6625	cg43927534	701	CCAGTCAGGGTCA ATGGCCCAGGA GA[A/C]GGGGT TCCCCACGATGA TGAGCAG	A	C	Leu	Arg (8796)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9E-148	1
6626	cg42929454	321	CTCTAAATTTTCCA CCAGAATCTTCA[ A/G]TTCTGTCTT GAAGCCATGGTA CACT	A	G	Ile	Thr (8797)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa.	1.1E-144	10
6627	cg43946394	239	ACACACTGAATC TGAGCTTCCGG AT[A]ACCGTAGC CCACGGGCACC AGCTTG	T	A	Ile	Phe (8798)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
6628	cg43946394	617	TGGCCAGGCCGA GCTCTTCTCCAG CA[C/T]GTTACGC CGGGCCTCCAG CTTGAG	C	T	Val	Met (8799)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19

6629	cg43324690	775	TGTACGAGAAAA ACAAAAAGGAAA TGCJAATATTCA ACAGCTCACCAA CTACA	G	C	Met	Ile (8800)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P22676 CALRETININ (CR) (29 KD CALBINDIN) - Homo sapiens (Human), 271 aa.	1.6E-143	16 (16q22.1)
6630	cg43024858	1114	TGTGTGTGTCT GACGGCTTCGAA GJA/GJACGGAA GATGCCCTGTGTG CCGCCG	A	G	Glu	Gly (8801)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa.	2.3E-142	22
6631	cg43935709	1680	AGATAAATGCCT TGGAAGTGGCAC AT/CJAGAAACAT TCTGATATTACC ACCAA	T	C	Tyr	Cys (8802)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
6632	cg43973762	594	CCAGGGGCTCA GTGAAGCTATGA ATT/GJAATTAGA TGCTGTTTCAGCG GGAATA	T	G	End	Glu (8803)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.2E-137	
6633	cg43973762	741	AGAGAAACATCT TGAGGAGCAGAT TGC/CJCTAAAGTT GATAGAGAATAT GAAGA	G	C	Ala	Pro (8804)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.2E-137	
6634	cg43948495	677	GCTCCCTGCTT GATGCGTCGTGT GJAT/CCTCGTCA AGCTTGGGCTG GTCCAG	A	T	Val	Asp (8805)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
6635	cg42923692	395	ACAGGAAGACCC AAGGTAACACAA TTC/GJACTTTCAT ATACCGAGAAAA GGACA	C	G	Ile	Met (8806)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to REMTREMBL-ACC:G298105 GAMMA- DELTA T-CELL RECEPTOR - HOMO SAPIENS (HUMAN), 260 aa.	3E-133	14 (14q11.2)

6636	cg43918679	613	CCCGTGCTGCG GCACACAGCCCC CAC[C/G]GCTAC CGCATGACCGTG CTGCGCAC	C	G	Arg	Gly (8807)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
6637	cg43918679	614	CCGTGCTGCGG CACACAGCCCCCA CC[G/C]CTACCG CATGACCGTGCT GCGCAC	G	C	Arg	Pro (8808)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
6638	cg42382358	835	CATGCAGCGG GGACGACGAC GGC[A/G]CGCTC CACGCCGCGCTG CCAGGTGCA	A	G	Thr	Ala (8809)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa.	5.7E-130	4 (4pter)
6639	cg44128041	215	CAGAAGGAGCT GCTGGAAAAGG GCA[A/G]CATCAC GCGCAGGGCA AGAGCCAG	A	G	Asn	Ser (8810)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
6640	cg43300586	705	CAGGGCACATTC GCCTCCCAGGT GAT[C/G]GCTGGA GGGGGACAAAGT TGAAAGTG	T	C	Met	Thr (8811)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa.	3.6E-128 (19q13.3)	19
6641	cg43949061	408	GCAGGCCACGC ACCACAACCCGG GC[C/G]TGGGGC TGTCGCTCATTC ACCAGTT	C	G	Gln	His (8812)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19

6642	cg43986720	2320	GGGCACACACTC CAGGCCCTCGTC A/C/TTCAGCAG CCCCCGCATCG CATCAG	C	T	Ser	Asn (8813)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
6643	cg43943363	167	AGTGTGCGGCA CCAGCAGGCAG CTG/G/C/CTCCG GCTTTGGGGTAT CTGGGCTC	G	C	Ala	Pro (8814)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P04179 SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) - Homo sapiens (Human), 222 aa.	1.7E-120	6 (8q25.3)
6644	cg43933691	286	ACTCTTCAGCAG CTCTCCTAGGGT C/A/G/TTCCCTCA CAACGTATATTC CGTTT	A	G	Met	Thr (8815)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
6645	cg43933691	881	CATCTTTTCTTT TCCTTCCTTTCT T/C/GTCTGAAGG TGTGCTGGACAC CTCC	T	C	Lys	Glu (8816)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
6646	cg42551270	472	GAAGTCTGTGCG GCAACCTACATG A/T/C/JGGGGAAT GAGTTGACCTTC CTAGAT	T	C	Met	Thr (8817)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P16410 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4-1 PRECURSOR (CTLA-4) (CD152 ANTIGEN) - Homo sapiens (Human), 223 aa.	5.4E-118	
6647	cg43067745	155	ATACACACAGAA AGAGATCACAGA C/T/G/CCCTACCT TAGAAGAAGGGA GGTGG	T	G	Ser	Arg (8818)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6648	cg43067745	164	GAAGAGATCAC AGACTCCCTACC T/T/GJAGAAAGAG GGAGGTGGTAG ATGAAA	T	G	Lys	Gln (8819)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	

6649	cg43067745	205	G TAGATGAAATG AACTGTATGAAG A[G]TCCACTAGC CTGGCCACACACA CAGAA	G	T	Ala	Asp (8820)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6650	cg43067745	227	A GAGCCACTAGC CTGGCCACACACA C[A/G]GAAGAAG GACTGGCCCGT CTTCTTG	A	G	Cys	Arg (8821)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6651	cg43067745	260	G ACTGGCCCGT CTTCTTGAAGCC CA[T/A]GCTCTGG TAGAGGCCATA GCAGAG	T	A	Met	Leu (8822)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6652	cg43067745	403	CTGACGACGGT GCTCACTGTCCA CA[G/A]JAGAGAT GAAACAGCTGCA ACCGCTT	G	A	Ser	Phe (8823)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6653	cg43919033	1675	CCCAGGCCAT GGTGACTAGGG GCA[G/T]AAGTAC CCAGAGAAAGACT GAGGTCC	G	T	Leu	Met (8824)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
6654	cg43926002	391	GGGCACAGAAA CACAGCAGCGG GAG[C/G]JAGCAA CACCAGCACTGC CAACAGAT	C	G	Ser	Arg (8825)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
6655	cg43268843	781	GACTGCTTCCAG GAAAACCTCTGA C[A/G]TGGTACTG AAAAGAAAGCAA ACTAA	A	G	Met	Val (8826)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43260 HYPOTHETICAL 25.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 218 aa (fragment).	9E-116	1



6656	cg43298119	420	TGTAGAATGGAT CAAAGCTAGAGT G/A/GCTGAGTT GAACCCAGACAA GAACTG	A	G	Thr	Ala (8827)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34039 CGI-44 PROTEIN - HOMO SAPIENS (HUMAN), 450 aa.	1.3E-114	
6657	cg43971133	312	GCTGAGGCGCG TCTTCGAGAAGT AC/A/GJGGCGCG TCGGCGACGTGT ACATCCC	A	G	Arg	Gly (8828)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
6658	cg43942219	293	TTTCGGCGCTGG GTCGCCCAAGC A/G/AJAATGGAGA CGGATAGAGTG GTGGCT	G	A	Ser	Phe (8829)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
6659	cg43942219	317	AGAATGGAGACG GATAGAGTGGTG G/C/AJTCGCCAGAA TCCCGAAGAACA TAAGC	C	A	Ser	Ile (8830)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
6660	cg43036790	114	TCAACAATCAA GAGAAAGTCATT CT/AJTGTAAGTGT AACATCTTCCTC TTCCC	T	A	Gln	His (8831)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
6661	cg43036790	152	TCITCCTCTCC CCATCGGGGTTG A/A/CJCTCTATTGA AATGTATACTGA AATCA	A	C	Phe	Val (8832)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
6662	cg43116651	752	TCTGTGTGGCAG AAGGATCAGCTG GT/AJGACACAG CTGCACCTGGCAA GAAAT	T	A	Val	Glu (8833)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa.	1.6E-109	2

6663	cg43325271	810	ATCCAGCCCCCAGT CCCCTGTCTTCC CTTAJGGCCCCCT CTCGCGAAGCAC CTGCAG	A	Leu	Gln (8834)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC: CAB43675 HYPOTHETICAL 97.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 892 aa (fragment).	1.5E-108	
6664	cg42657906	257	GAAGGGTGTCTG GGGGGCTCTGA AAGTAAJGGGCA GAGGGGTGGCT GGCCITGGGG	A	His	Leu (8835)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC: Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11
6665	cg43976960	634	TGGCTGGAGACA ACACTTTATCAG TTTCTTGACACT GACAGGAGTGG AACAGT	C	Phe	Leu (8836)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
6666	cg43967668	470	TTCCTCCGAGCCA GTCTGAGGGGT GCCTTCAGGGT GCCCCCGCGCG AGATGCAG	T	Gly	Ser (8837)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
6667	cg43959985	1027	GTCGTTGGAGTC CACTTTGTCTAT GAAJGGTAAAG GTACGTCCTCTG GCTCAT	A	Leu	His (8838)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC: O43329 HYPOTHETICAL 23.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	2.4E-106	16
6668	cg43932706	197	AGAGATTGATAT TCGTTTGAGAGA GAAJGAAATTTCT AAAATGTGTTTT GAAAC	G	Lys	Glu (8839)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC: BAA82992 KIAA1040 PROTEIN - HOMO SAPIENS (HUMAN), 544 aa (fragment).	5.2E-104	
6669	cg43941552	757	CGGCCTTCCTGA GGCATGGCCGT GAAGJGACCCCT GTGTGGCGAGG TGCCGCTC	G	Asn	Ser (8840)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC: P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	

6670	cg43252708	486	CGACCTCAGGA GCGTCCGAAGT GGG[C/T]TCATCA CACAGAAATCGGC AAGACCT	C	T	Leu	Phe (8841)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75879 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
6671	cg43049606	457	CAGAAGGAAAGT CAAGTTTACTTG TT[G]GGAACT GGACTCCGAGG GAAAGAG	T	G	Leu	Tyr (8842)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13094 SLP-76 TYROSINE PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 533 aa.	4.3E-100	5
6672	cg43941550	525	GAGCGGCACCT CGCCACACACAGG GTG[C/T]TCACG GCCATGCCCCAG GAAGGCCCGG	C	T	Ser	Asn (8843)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
6673	cg43941550	669	CATCTGGAAGTT GTGGACTTTTCT A[G/T]TGAGAGC CTCAAGACTGGG GATGCT	G	T	Thr	Asn (8844)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
6674	cg42903839	211	GGACCGGCGGC CCAAGCTGTGGA GAC[G]GCCGGG CTGGAAGGCC GGAGGACG	C	G	Thr	Arg (8845)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6
6675	cg42903839	717	GTCAAATTGCTT AATAGAAATAAT GAC/JAGTGTGG TTGATTCAAAA AATGAA	A	C	Glu	Ala (8846)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6

6676	cg43971745	1964	CTCTTATCTGGG AACAGTGCCAGC TGGTGTGGGCA GCCAGT	G	T	Gln	Lys (8847)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
6677	cg43992729	709	CCTGGGCCATAT GTTGCTGGGAAT TTC/TCCTCCACC CTTCGTCATGCA GTGGA	C	T	Pro	Ser (8848)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa.	2.6E-95	14
6678	cg43927693	667	CCCCTACCTGGC CTGGCTGGCCTT C[G/A]CGACCAC ACTCAACTACTG CGTATG	G	A	Ala	Thr (8849)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
6679	cg36896591	81	TCCGGAGCCATG CAGGCCGAAGG CC[G/A]GGGCAC AGGGGTTTCA CGGGCGAT	G	A	Arg	Gln (8850)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75637 LAGE-1A PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	6.8E-95	
6680	cg42914758	224	ATTCACCAGTTC TGGATGAAAGAC TGG/CJATGTTGAT TTATGCAGCCAT TTTAG	G	C	Ser	End (8851)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88422 UDP- GALNAC:POLYPEPTIDE N- ACETYL GALACTOSAMINYL TRANSFER ASE T5 (EC 2.4.1.41) - RATTUS NORVEGICUS (RAT), 930 aa.	7.8E-94	
6681	cg42907594	354	GCCAATAATGCA ATCAGGGTTTCT TTC/AJATCAGGAG CTTTGACCACCA CCTTG	C	A	Glu	End (8852)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa.	3.8E-92	17

6682	cg43964799	743	TACAACAAGACT ACAATGCTTCTC T[C/A]CAAGCAAT TCGTGCAGTGG GATGAG	C	A	Ser	Tyr (8853)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75935 DYNACTIN SUBUNIT - HOMO SAPIENS (HUMAN), 186 aa.	4.9E-92	9
6683	cg43921592	158	AGGCTGGCTCA GGACTATCTGCA GT[G/A]CGTCCTA CAGATACCACAA CCTGGA	G	A	Cys	Tyr (8854)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
6684	cg43921592	219	GCAAAACGTCCA GAGTGCTACAAA A[T/G]GTTGCGTT CTCAGTCCAAAA AGAAAG	T	G	Asn	Lys (8855)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
6685	cg43987971	403	AGCTGCAAGCGA ATGAGGTAGAAT G[G/A]ACACAGA CATGAGATAGAC ATCAGC	G	A	Pro	Ser (8856)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa.	7.2E-91	1
6686	cg25236776	881	CAGTGCCTCCCC TGCGGCCCCGG GG[G/A]CAAAGG CCGCTGCTTCGG GCCCAGC	G	A	Gly	Asp (8857)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.2E-91	
6687	cg43978148	707	TGTAGCCCATGC TGTTATCAAGC A[A/G]TGCTCAGC TTGAAGAATATT CCTGT	A	G	Met	Val (8858)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16

6688	cg43978148	815	CCTGCACAGTCT GCAACTTCTCTGA G[G]CCTCTGTCT GAAATAAACAT GAGGC	G	T	Ala	Ser (8859)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16
6689	cg43963913	707	CAAGTCCGATC CCACCAGGACTG G[A/G]AGACTCG CGTCCAGCTGGA GCTTTG	A	G	Phe	Ser (8860)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
6690	cg43922714	416	CCTCGCTGGATC AATCGACTTGCC T[A/G]CTTCAGCT CCTGTATACGCT TTCTA	A	G	Tyr	Cys (8861)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa.	9.8E-87	19
6691	cg43068353	208	CCTGGTCTGCT GCTCCGGGGT CT[C/T]GGCTGC CAAAC TGAATC CTTCTCC	C	T	Arg	Gln (8862)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
6692	cg43068353	391	TTTCTTTTCTTGA TTTCTCTGGTTCC[ G/A]AAATGCCAA ATTAAATCCATC AGC	G	A	Ser	Leu (8863)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
6693	cg44018226	1252	CCCTGCAGGCAA TTACTCTCACCG GT[A/G]GGTAAAA TCAATCGCAGCA GAGAA	T	A	His	Leu (8864)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
6694	cg36842490	547	GGAAAACGTGTT AGCAGTAACATC TTC/TAGAAAGACC CTGTACCAGTCA AACGT	C	T	Ser	Leu (8865)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa.	2.3E-85	

6695	cg36842490	606	TGCAGTCTTCAC TGACAACTATAC C[C/G]GCCCTTAG AAAACAAATGGC TGTAAG	C	G	Arg	Gly (8866)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa.	2.3E-85	
6696	cg43142459	281	GGGTGGTCACC CTCCAATACAAT AA[G/C]ATGCCA GGAAGAGTAAGT TGCCCTT	G	C	Ser	Cys (8867)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15205 DIUBIQUITIN - HOMO SAPIENS (HUMAN), 165 aa.	1.9E-83	6
6697	cg43969140	348	GCCATCTGGTTC CACATTCAGGGC CT[AT]CACTATG CCATCCTGTACC ACCAT	T	A	Lys	Met (8868)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6698	cg43969140	441	CGAATCATCTAG TAATAAGTCTGT CT[G/C]CTTCCCA AAGGCCCCAGT GGGATC	T	G	Glu	Ala (8869)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6699	cg43969140	730	GGCTCCCTTCA AACACCTCCACT G[C/A]TGGGATG GCATCTCCCAAC TTGATT	C	A	Ala	Ser (8870)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6700	cg43989505	634	ATCAGCGGCTCT TTGTATGATGAC G[AT]AAGGATGA GGCGGCAGGGA AGAAGA	A	T	Glu	Val (8871)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75274 F16601_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 158 aa (fragment).	2.2E-80	
6701	cg43969316	745	CAGCAGCTGAG CTTGAATCAGCA CA[G/A]CCGAGC CTTTAATATCGA AAGAGCG	G	A	Ser	Asn (8872)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.5E-79	5

6702	cg42331787	384	TCATCCCGCGTG CTCCGGACACAA TTC/ACTTTTTC GCAGTGGATGC CTGCAA	C	A	Arg (8873)	Ser (8873)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75951 LYSOZYME HOMOLOG - HOMO SAPIENS (HUMAN), 148 aa.	7.5E-78	17
6703	cg44936941	897	TTAAGATAATATA TACATGTCACAC A/GTCTTCCATC TCCATTTGGATT ATCA	A	G	Cys	Arg (8874)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
6704	cg42462901	430	ACTTTATTGGGG AACTGTGGAAT TTT/CJTTCAGGCA ACTCAATAAAAT GGGTG	T	C	Lys	Glu (8875)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83043 KIAA1091 PROTEIN - HOMO SAPIENS (HUMAN), 1359 aa (fragment).	1.4E-75	
6705	cg43989639	955	ATGCCCCAGACCC ACTCTGCAGTAA G/G/CJTGTTCACAA AACAGAAATGCG ACAAA	G	C	Pro	Ala (8876)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1 - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
6706	cg38276737	336	AGACCTCAATGA CAAGAGTGTGCA G/T/CJGTGCCCT GGACTTTGCCAT CAGCGA	T	C	Cys	Arg (8877)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P28325 CYSTATIN D PRECURSOR - Homo sapiens (Human), 142 aa.	3.1E-74	
6707	cg44004729	520	AGTTTCTCCGGC CACGAGGCCCT GGG/AJTAACCT AGACTGATACCT CCTCAT	G	A	Thr	Ile (8878)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	
6708	cg43933021	621	ACAGCTATCAAA CTTCTACCACT CTT/CJCTGCTGGT CGACGTCGGCG TCTGGC	T	C	Arg	Gly (8879)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13



6709	cg43932428	597	GCTCGATTTTGC CAAGCACCTGGT TJA/CJTGGGTAT GGCCCGTCCGC TCTCAT	A	C	Asn (8880)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	
6710	cg42691635	483	TAGAGAGAGTTG ACGGTGTCTCG TT/CJGGGTGG TCGTTGCTGATT TTGAAA	T	C	Gln (8881)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16378 PHL E1F1 - HOMO SAPIENS (HUMAN), 134 aa.	1.8E-71	12
6711	cg43271682	339	GGGGCGGACA GGCCCGCTGC TGG[G/C]GGCTC CCGGAGCTCTC GGGGGGCGG	G	C	Pro (8882)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
6712	cg43917616	146	TTGGCAACTTTT GATGCATTTTC GJA/GJTITTTGGTT CCCAGAGGGCA TTTTT	A	G	Ser (8883)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13901 C1D DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 141 aa.	6.9E-70	
6713	cg43942922	229	TGAGCCCACTC TCAGGCCACTAG G[G/A]GCAGAAC AAATAGGTCCTC TGTCAA	G	A	Ser (8884)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6714	cg43942922	265	TAGGTCCTCTGT CAAGACCCCTGA AJA/CJAGTTGTC CCCACAGCCCCT GAGCT	A	C	Thr (8885)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6715	cg43942922	362	TCTCAGGCCACT AGGGGAAGAAAA AJA/GJTAGGTCCT CTGTCAAGACCC CTGAA	A	G	Ser (8886)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	

6716	cg43942922	407	CCTGAAACAGTT GTGCCACAGC CC[C/T]TGAGCTC CAGCCTTCCACC TCCACA	C	T	Pro	Leu (8887)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6717	cg43942922	437	CTCCAGCCTTCC ACCTCCACAGAC C[AG]ACCTGTCA CCTCTGAACCCA CATCT	A	G	Gln	Arg (8888)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6718	cg41400057	447	CACCTGGCCTGA ATGCAGCATGGG G[G/C]TTTTGGCT GGCAGCAGTGAT TGTTG	G	C	Pro	Ala (8889)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa.	2.7E-68	9
6719	cg43955219	980	GGATCCTCAAAA CTCAGAACGTGG C[C/T]GGGCGTG GTGGCTCACGC CTGTAAT	C	T	Arg	Trp (8890)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
6720	cg42831353	787	TGCACCGCGC GGTGGTGAGGA CAC[AG]GGCTG CGGTGTAAGCCC GCGTCACC	A	G	Cys	Arg (8891)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.3E-67	22
6721	cg43927424	353	TCCCTGTCTGCA AGTCGGGCAGG AA[C/T]AGAAACA CACCTACCTGCC ACTAGA	C	T	Gln	End (8892)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6722	cg42381630	244	GAGTTGGCGAG GAAGATCGACCT ATT[C/AT]TGCC TAGACCAAGGCG CTATGT	T	C	Tyr	His (8893)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	

6723	cg42381630	439	AGGTCAAGGC CGAAGCCTGAAG CTC/GJATAGCCA GGAACAGGGTC ACCCACA	C	G	His	Asp (8894)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
6724	cg43950549	273	CTTATTGTCACA TTCTTCTTGGGA A/A/TTACAGTGT TGCTGTTGCTGA TGCAA	A	T	Lys	Asn (8895)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6725	cg43950549	485	CAAGAACTTCAG AATGGGTCAGAA T/A/CJGGAAGTG GTGATGGAACCA GCCCTG	A	C	End	Ser (8896)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6726	cg43308257	773	GACCCGTGACCC CTGTTCAAGATC T/A/GJGTGGCG GAGCTGATCCAG CAGCTG	A	G	Tyr	Cys (8897)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
6727	cg42686636	719	GGTTATACCACA AGCTGTGCTTGC A/A/TJTGAGACT GAGCAAAAGGAA ATGTG	A	T	Gln	His (8898)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O08904 BRAIN X-LINKED GENE (BRX PROTEIN) - MUS MUSCULUS (MOUSE), 216 aa (fragment).	4.4E-59	
6728	cg42566513	351	TTCTACCCCTGAG TGCGAGATAAGA A/C/TJGATGGGT GGAAGAGAGCA ACGCCAG	C	T	Thr	Met (8899)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70576 NUCLEAR PROTEIN SA3 - MUS MUSCULUS (MOUSE), 1240 aa.	9.6E-59	
6729	cg43930685	1007	CAGCGATTCTTT TTTTGTTTCGGTT T/A/TJTCAGAGA CTTGCTTTTGCTC TTCA	T	A	Lys	End (8900)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	

6730	cg43930685	821	GGAGTCAAATC TTTTGGATCTTT [C/T]ACCAACAAC TACTGGATTTC TTTT	C	T	Glu	Lys (8901)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
6731	cg40968986	251	TGTGCAGATGAA GGCCAGTGAGC TG[G/A]JAGCAGG AGCAAGAGAGA GAGGGCTC	G	A	Glu	Lys (8902)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6732	cg40968986	267	AGTGAGCTGGA GCAGGAGCAAG AGA[G/C]JAGAGG GCTCCAGAATCA TTGCCAG	G	C	Arg	Thr (8903)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6733	cg40968986	372	AGCAGATCAGG GGGTGTGGTGA AGA[A/G]CAACTT TGTGCCCCACCAA TGTGGGT	A	G	Asn	Ser (8904)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6734	cg43934461	766	TCGGGGACCCC AAGAGAAATTCAT AT[G/T]CTGGTGG ATTGGTGTGAGG CACCCG	G	T	Ala	Glu (8905)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa.	8.8E-57	3
6735	cg43968980	1126	TGCTTCCTTGGA CTGAAGAATAAA C[A/C]TTCTTCCT ACACCTTCATAC ATGTT	A	C	Met	Arg (8906)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
6736	cg44011808	554	AACCACATGAGT CCGCTGAAGAAC T[C/T]GCTCTGGA ACACCTGGGATC TGGTC	C	T	Glu	Lys (8907)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa.	2.5E-56	

6737	cg43916991	120	GACATCTGGCCA GGTCCATCTCTG A/C/TJCGGCTCCT GGTCAACCCCCA GGGAG	C	T	Thr	Ile (8908)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
6738	cg43916991	74	AATGTGGGGAAG TGTGGATGTTAG CT/GJCTGAGATT GGGGTGTGGTC AGACAT	T	G	Ser	Ala (8909)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
6739	cg39695368	203	CGGGATGGCTTA CATTGATATCAT C/A/GJTACGTAG GTCCTTCTCATA GATGTC	A	G	Met	Thr (8910)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33910 HYPOTHETICAL 21.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	1.7E-50	X
6740	cg40357240	240	ACCGGATGTCTT CGGCCAGTGCT GA/A/GJGGGAC TGACTGGGGATA CAGCTTT	A	G	Leu	Pro (8911)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment).	5.4E-50	
6741	cg44917490	1621	GGGACCGTTTCC TCTTCTCTTCA G/C/gap/CTGCGG AGGCTCCACGAA GTAATCA	C	gap	Ala	Leu (8912)	FRAMES HIFT	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0	19
6742	cg44917490	873	GGGGTGTTCAT CCTTGGAATCTG GA/G/gap/GCTGC AGCCACCCCTTG TCCTCGCT	G	gap	Pro	Leu (8913)	FRAMES HIFT	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0	19
6743	cg42663825	2303	GACAAAACACTG TTTGTTGGGTTTA C/C/gap/GCCCCC TGCAGATCGCCT TGCCATC	C	gap	Pro	Arg (8914)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2406580 NUCLEAR VCP-LIKE PROTEIN NVLP.1 - HOMO SAPIENS (HUMAN), 750 aa.	0	1

6744	cg43987714	2730	TGGTTACGTTTG ATGAGGAGCTGC G[G/gap]CCATTG CCAGTGTCTGTC CGTGTGG	G	gap	Pro	His (8915)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
6745	cg43987714	2785	GGCAGTGGATGT GGTGGGCCAGG CT[G/gap]GCAAG CCGAAGACTATC ACAGGGTT	G	gap	Gly	Ala (8916)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
6746	cg43987714	2786	GCAGTGGATGTG GTGGGCCAGGC TG[G/gap]CAAGC CGAAGACTATCA CAGGGTTC	G	gap	Gly	Ala (8917)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3

6747	cg43987714	2914	CCCCATTCCTGGA C AGGTTTTGTTAT C[C/gap]JTCGGA AGAACCCCAATT ATGATCT	gap	Leu	Phe (8918)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.[pds:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
6748	cg43277632	1676	GCAAATATCGGT G GTCTTTGGCCGA A[G/gap]GGACTG CAACAGTCTTT ATAATCC	gap	Gly	Gly (8919)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
6749	cg43933946	1781	AGCCAAATCCCA G GAGTGCTGGTG GG[G/gap]CCAGG CCAGTGTCAGAT TCITTAAT	gap	Ala	Ala (8920)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.2E-231	7
6750	cg43958825	343	GGATCTGCATGA C TTCTGGCCCGG GC[C/gap]TCCTC ATTGGGCATCGG GAACCTCA	gap	Glu	Glu (8921)	FRAMES HIFT	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
6751	cg43933600	1192	TGCCCCCGACG G AAGATCCACTTC AG[G/gap]CTGCG CTGCTCGATGAT GTTGCTAA	gap	Ser	Ser (8922)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19
6752	cg43933600	348	CGCACCTCATGG G GGTAACAGCGG CA[G/gap]CTTCA CGATGTGGAAGT CTTCATAC	gap	Leu	Cys (8923)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19

6753	cg43933600	556	CATACAGGGACA GGAACCTCAGCAA T[G/gap]CATACG CAGATGAAAGTT GTCTGCT	G	gap	Cys	End (8924)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19
6754	cg43916747	1057	GAATCCGGGGC ACCAGCTACCAG AG[C/gap]CCTCA CGGCATCCCCAT AGACCTGC	C	gap	Pro	Leu (8925)	FRAMES HIFT	ATPase_ associate d	Human Gene SPTREMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa.	4E-163	19
6755	cg43947105	1581	AGAGCAAGATCA AACCCAGCTCT T[G/gap]GCGGTG CGCCCCAGGAAT TCTCCGG	G	gap	Ala	Ala (8926)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
6756	cg43947105	1582	GAGCAAGATCAA ACCCAGCTCTT G[G/gap]CGGTGC GCCCCAGGAATT CTCCGGT	G	gap	Ala	Ala (8927)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
6757	cg43927442	1437	CACAGCAAATTT GTTCTCTAGGGG G[G/gap]ACCACT TCACAAAAGTAG CTGCGCG	G	gap	Ser	Ser (8928)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. Jcdls:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.4E-146	17



6758	cg43927442	653	TCACCTCAGCTTC ACATTATCCGA G[G/gap]CCCCTGG ATGGAAGACTCG AGGGTCT	G	gap	Gly	Gly (8929)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.   pcds:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.4E-146	17
6759	cg43967912	1267	AGCTGCAACAC CCGGCCACGCA CT[gap]TGCACA TACTGCGAACTA TCACTTGA	gap	T	Gln	Gln (8930)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.6E-108	8
6760	cg43304881	1413	CAGGGCCAGCT GCCGGAGGCGC TCC[C/gap]TGGC GTCACGGTTGCT CTCGGAGGA	C	gap	Arg	Arg (8931)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q19335 F11A10.2 - CAENORHABDITIS ELEGANS, 610 aa.	8.7E-94	
6761	cg43132502	208	GGCAGGAGGCA GGAGTTGGCGAT GC[C/gap]ACCTG GGGTCACATTG AGTCTGGA	C	gap	Pro	His (8932)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6762	cg43132502	309	CAGGGAAGAAG GGGAGGCGCCA GAG[G/gap]CAGG GCCATGCTTGGC TTCCACAGCT	G	gap	Ala	Gln (8933)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6763	cg43132502	346	TGGCTTCCCAGC TGGCCCCCAGTG CA[gap]A]GTGGG TGGCACCCGCCG AGGCTGCTG	gap	A	Gln	Gln (8934)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11

6764	cg44015998	469	TGGCTGTTGAAG TCGGGCGAGGA GC[C/gap]GAGGA GCAGGCCAATGA TGGCCAGG	gap	Gly	Ala (8935)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.5E-53	
6765	cg43918042	1862	GCTGACCCTGC GAGTGCGCGAC GGC[gap]GJCGGA CCCGCTCGCTCC TCGCAGGCC	gap	Ala	Ala (8936)	FRAMES HIFT	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
6766	cg43918042	2009	ACCCCCATCCTG CAACTGCGCGCA G[C/gap]CGACTT GGACGTGGGG TCAACGGG	gap	Ala	Ala (8937)	FRAMES HIFT	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
6767	cg43957225	2825	TTGCTACATAGC AGGTGCCAACTG G[G/gap]TCCTTT TCTGGTGTCGGT TTAAGAG	gap	Asp	Asp (8938)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0	10
6768	cg43957225	2832	TAGCAGGTGCCA ACTGGGTCCTTT T[gap]TJCTGGTG TCGGTTTAAGAG TTCTCCA	gap	Glu	Glu (8939)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0	10
6769	cg43977440	3175	GCATCACACTGC CACCAGAGCCCTC TTG[gap]CCCCCT GGGCAAGGGGC ACACGGAC	gap	Gln	Arg (8940)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P11215 CELL SURFACE GLYCOPROTEIN MAC- 1 ALPHA SUBUNIT PRECURSOR (CR-3 ALPHA CHAIN) (CD11B) (LEUKOCYTE ADHESION RECEPTOR MO1) (INTEGRIN ALPHA-M) (NEUTROPHIL ADHERENCE RECEPTOR) - HOMO SAPIENS (HUMAN), 1152 aa.	0	16 (16p11.2 )

6770	cg44026834	1087	CGGCCGCTCGC ACCGCGGCTCCT GC[C/gap]AGCTC ACTCTGAGAGAT GTGGGCCC	C	gap	Trp	Cys (8941)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6771	cg44026834	1320	GGGGCACGTGT GGGCTCAGGTG GGT[G/gap]CCAT AGGCAGCAGCA CTGGTCGTGG	G	gap	Gly	Gly (8942)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6772	cg44026834	1433	TGCTCAGTGTC TCGGAGACGCT GG[G/gap]CCTCT GGCTGCCCGAT GGAGAGCGT	G	gap	Pro	Pro (8943)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6773	cg40310734	1060	CTCAACACACTACA GAATATGTCGTC G[G/gap]TGCCCC CACTTGGAGCTG GACCCCTG	G	gap	Gly	Val (8944)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
6774	cg40310734	3291	CTTCTTCAAGCG GAACCGGCCAC CC[C/gap]ITGGAA GAAGATGATGAA GAGGGGGA	C	gap	Leu	Trp (8945)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
6775	cg42558238	2563	TCCTCAGAGATG CAGAGACCTCC C[C/gap]GGACTG CGATGACACGGT CACTTAT	C	gap	Pro	Arg (8946)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. pcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1 )

6776	cg42558238	2567	AGAGATGCAGAG ACCTCCCCCGGA C[gap/C]TGCGAT GACACGGTCACT TATTCAG	gap	C	Cys	Leu (8947)	FRAMES HIFT	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. pcis:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
6777	cg43303099	1216	TCTTGCACAGGA ACAGTAGCGTCC A[G/gap]CTGCGA GTCTGTATGGT CCCAAAA	G	gap	Leu	Cys (8948)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa.	8.7E-158	19 (19p13.3)
6778	cg42528468	283	TGCTCCTGCCTG GGAACAACCGG AA[G/gap]GTGTA TGAACCTGAGCAA TGTGCAAG	G	gap	Val	Cys (8949)	FRAMES HIFT	cadherin	Human Gene Similar to SWISSPROT-ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa.	8.4E-78	19 (19p13.3)
6779	cg43976467	882	TGGTGGTCAACA TAAGTGACCTGG G[G/gap]TACCCT AAGTCTTTGCAC ACGCTTG	G	gap	Tyr	Thr (8950)	FRAMES HIFT	cadherin	Human Gene Similar to TREMBLNEW-ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	1.2E-64	13
6780	cg43307361	1212	CACAGGCACTAG GGAAGGCGGCT GC[C/gap]ACATA GCGCCTTCTCC CTGCAGGG	C	gap	Val	Val (8951)	FRAMES HIFT	carboxylase	Human Gene SWISSPROT-ID:Q16822 PHOSPHOENOLPYRUVATE CARBOXYKINASE, MITOCHONDRIAL PRECURSOR (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-M) - HOMO SAPIENS (HUMAN), 640 aa.	0	14

6781	cg43264626	637	CATCTTGGGAA GCTGGCCAGGTT G[G/gap]CAATGC CACAGCGGTTGT TCTTATT	G	gap	Ala	Ala (8952)	FRAMES HIFT	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
6782	cg43264626	642	TGGGGAAGCTG GCCAGGTTGGC AAT[G/gap]CCAC AGGCGTTGTTCT TATTCGAG	G	gap	Gly	Gly (8953)	FRAMES HIFT	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
6783	cg42094324	596	AGATGTTGTGAA GGTCCTGGGCC TG[C/gap]CCACC CAGGAGCCAGC ACTGGGGAC	C	gap	Pro	Pro (8954)	FRAMES HIFT	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	2.1E-147 (19q13.2 )	19
6784	cg43970982	2435	GGGATAGTTGGA CAGAAGGGAGA CC[C/gap]TGGCT ACCCAGGACCA GCTGGTCCC	C	gap	Pro	Leu (8955)	FRAMES HIFT	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6785	cg43011543	1879	TGATGGCGTGA AACCCCCCATG C[C/gap]TACGGG GGCTAAGAAAGG CAAGAAT	C	gap	Tyr	Thr (8956)	FRAMES HIFT	collagen	Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
6786	cg43998782	110	ACCTGATTGTGG TGACCGACGGG CA[C/gap]CCCCT GGAGGGCTACA AGGAACCCT	C	gap	Thr	Thr (8957)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	

6787	cg43998782	138	CCTGGAGGGCT ACAAGGAACCCCT GT[G/gap]GGGGG GCTGGAGGATG CTGTGAACG	G	gap	Gly	Gly (8958)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6788	cg43998782	144	GGGCTACAAGG AACCCCTGTGGG GGG[G/gap]CTGG AGGATGCTGTGA ACGAGGCCA	G	gap	Leu	Trp (8959)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6789	cg43998782	446	GACCCCGGCTTT GAGGGAGAACG AG[G/gap]CAAGC CGGGCTCCCA GGAGAGAAG	G	gap	Gly	Ala (8960)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6790	cg43998782	66	GGAGCAGCTCCT CGTGGGGGGCT CC[C/gap]ACCTG AAGGAGAATAAG TACCTGAT	C	gap	His	Thr (8961)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6791	cg43991318	3976	CCCAATGACACA GATCTCTCCTGG C[C/gap]GGCCGT CCCGGCCTGGC TTTCCCGG	C	gap	Arg	Gly (8962)	FRAMES HIFT	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73 1 (1p34)	
6792	cg43938820	1581	TCCTCTTGGCAG CGCGAGACGAG GC[C/gap]TCGCG GTAGAGCGGG TCACATAGC	C	gap	Glu	Glu (8963)	FRAMES HIFT	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5E-59 (21q22.3 )	21

6793	cg43063256	258	TGGCATCTCTG TCACATTGGAA A[A/gap]TGAAGA ATCCAGGACAT GGGCTTG	A	gap	Met	End (8964)	FRAMES HIFT	complem ent	Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.   pcis:SWISSPROT- ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0	1 (1p32)
6794	cg43933757	2462	CAGACGATGTCT GAGTGTGAGGC GG[G/gap]CGCTC TGAGATGCAGAG GGCAGAGC	G	gap	Gly	Ala (8965)	FRAMES HIFT	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
6795	cg43029289	1158	CCTATTACTGTG ATGAACATTTTG A[gap]A/GACTCC GTCAGGAAAGTTA CTGGGAT	gap	A	Glu	Glu (8966)	FRAMES HIFT	complem ent	Human Gene SPTREMBL-ID:Q14570 COMPLEMENT FACTOR H PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	6.4E-265	
6796	cg21644442	1562	TAACCTCCGTTCC TTTGACTGACAC A[G/gap]GCCATG AGAGGCAGTCC GAGGGATC	G	gap	Gly	Ala (8967)	FRAMES HIFT	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5E-304	1 (1p21)
6797	cg21644442	1563	AACTCCGTTCTC TTGACTGACACA G[G/gap]CCATGA GAGGCAGTCCG AGGGATCC	G	gap	Gly	Ala (8968)	FRAMES HIFT	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5E-304	1 (1p21)
6798	cg43920512	779	CCTAGGGAAT GGAGGTTAAATG TT[A/gap]AACCTAA AGTGGGTACAT GAAGAA	A	gap	Lys	Asn (8969)	FRAMES HIFT	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.1E-231	4 (4q27)

6799	cg43996855	4913	CAGGGCCTGGT GGATGGCGCG TCG[C/gap]CATT CAGCACCACTAT GGGCGAGCT	C	gap	Gly	Ala (8970)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6800	cg43996855	4941	TCAGCACCACTA TGGGGCAGCTG CC[gap]CJAGGCG GATCTGGAAAC GTCGCCGT	gap	C	Gly	Gly (8971)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6801	cg43996855	5050	TCCGATCAGTGG CCACGCAAAACG GG[C/gap]CCGGG GGCGCGGACCG GAGCTGCCG	C	gap	Gly	Ala (8972)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6802	cg43996855	5205	GGTCGTTCCGG CTGAGGCTGGT GCC[C/gap]ATGC TCCGGGGAGGT GCGGTTTCCA	C	gap	Met	Met (8973)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6803	cg43315849	1727	CAAGGAAGGGC AGGCGCCAGGG CCC[C/gap]GGCG GGTAGTTCTTTG GGCGCCGTC	C	gap	Pro	Pro (8974)	FRAMES HIFT	cyto450	Human Gene SWISSNEW-ID:P51589 CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYP11J2) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa.   pcis:SWISSPROT- ID:P51589 CYTOCHROME P450 1IJ2 (EC 1.14.14.1) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa.	7.2E-257	1 (1p31.3)
6804	cg43966704	905	CGCTGTCTCCTC TCCACAGATGTA GG[gap]CCCCAG CCCCGCGCACC ACAAACAC	G	gap	Ala	Ala (8975)	FRAMES HIFT	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11



6805	cg43966704	134	GGTGGTGGGCT AAGAGGCAGCCT GC[C/gap]GGGCC TGATGCTGCTGG GCAAACCG	C	gap	Arg	Arg (8976)	FRAMES HIFT	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
6806	cg42717303	320	GGGGATTGAGC GTAGAATGGCGT AT[G/gap]CAAAT AGGAAATATCAT TCGGGTTT	G	gap	Ala	Asp (8977)	FRAMES HIFT	cytochro me	Human Gene SWISSPROT-ID:P00158 CYTOCHROME B (EC 1.10.2.2) - MUS MUSCULUS (MOUSE), 381 aa.	1.4E-175	
6807	cg43935752	1098	GCCCCAGTGAC CATGAAGAGTGA GG[gap/G]CTGCA GCCAGGGAATA GTCCATCGC	gap	G	Ser	Ser (8978)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa.	4E-82	11
6808	cg43935752	1238	TGGAGCCAGAAT GGTGGCTCGGT GA[C/gap]AAGTG TATGTGCTGCAC TCCACACC	C	gap	Leu	Phe (8979)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa.	4E-82	11
6809	cg43962888	502	CCATACAATGTA CTGGCCCCAAAG G[G/gap]AGCTTC AGGCACCAGGG AAGACCCCT	G	gap	Gly	Glu (8980)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSPROT- ID:P10808 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
6810	cg43962888	627	GTTTGGCTGCA CAAAGCGGAGG CC[C/gap]AGCGA TGCCCCCGCTGT GGAGCCCA	C	gap	Gln	Ser (8981)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSPROT- ID:P10808 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)

6811	cg43941766	557	GCCATGGGCGC CACTCGACATAG GC[C/gap]GCCCC AGCTGTGGCG GGACCGACC	C	gap	Arg	Arg (8982)	FRAMES HIFT	cytochrome	Human Gene Similar to TREMBLNEW- ID:E1248288 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 109 aa.	1.5E-57	6
6812	cg43958586	144	TCTTCTGGTCA AAATGGCTGGTA A[G/gap]CAGGCC GTTTCAGCATCA GGCAAAGT	G	gap	Gln	Arg (8983)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSPROT- ID:P14927 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (EC 1.10.2.2) (COMPLEX III SUBUNIT VI) - HOMO SAPIENS (HUMAN), 110 aa.	5.2E-57	8
6813	cg43923430	2583	GCCACTGTTCCA CTGCAGACCAG GA[G/gap]CCATC GGCCACACCACC CGCTCAGCA	G	gap	Leu	Ser (8984)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.7E-54	10
6814	cg42719440	383	TTGAGCATGCTC ACTCCCACCCCG G[G/gap]CAGCGC CACGAAAGTAGGT GAGGGCC	G	gap	Pro	Pro (8985)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSNEW- ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa.lpcis:SWISSPROT-ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa.	1.3E-51	
6815	cg43967318	1787	GACCAAGGCC CCCAGCTCCTTG AG[G/gap]CCCTG CCAAGTGGTCTC CTCCACCA	G	gap	Gly	Gly (8986)	FRAMES HIFT	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
6816	cg43967318	336	CTGCCAGGGGT CAGACTGCAGG GCG[G/gap]CCAT GCCCTCTCGGAT CCGAGCTGC	G	gap	Ala	Ala (8987)	FRAMES HIFT	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17

6817	cg43967318	417	TTTCTCATGCTG GGCCGTGGGT GG[C/gap]CCTCA CTCAGGGATCTT GAGGCCCT	C	gap	Gly	Ala (8988)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6818	cg43967318	419	TCTCATGCTGGG CCGTGGGTGG CC[C/gap]TCACT CAGGGATCTTGA GGCCCTCG	C	gap	Glu	Glu (8989)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6819	cg44028421	390	TCGAAGGTCACT GTCTTGACCCGC A[G/gap]GTACTC GTTACAGAGCCGC CTCTCCT	G	gap	Leu	Cys (8990)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P28037 10-FORMYL-TETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa.	0	
6820	cg44028421	391	CGAAGGTCACTG TCTTGACCCGCA G[G/gap]TACTCG TTCAGAGCCGCC TCTCCTA	G	gap	Tyr	Tyr (8991)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P28037 10-FORMYL-TETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa.	0	
6821	cg43962405	1134	ATGGGAAGACGA TTGAGGCTGAGG C[C/gap]GCTCAT GGACCCGTCAC CCGCCACT	C	gap	Ala	Leu (8992)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P48735 ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+- SPECIFIC ICDH) (IDP) (ICD-M) - HOMO SAPIENS (HUMAN), 452 aa.	8.2E-249	15 (15q26.1)
6822	cg43255016	1088	ATTAGGATTTTA GCCAGTAGTTTTI G[gap]GGTCAAG CCCTAACCTGAT TCCAAG	G	gap	Pro	Gln (8993)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.4E-156	

6823	cg43969759	949	GCAGCAACACCT ATGATGGCTGTG G[gap]CTTCAC CAGCCTCACCAC CTCCTCC	G	gap	Pro	Pro (8994)	FRAMES HIFT	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6824	cg44000219	741	GCACTGCCTGCC CTACTTCGCAA G[gap]GJCGCAGG GCCACGAGCTG GGCGCCAC	gap	G	Ala	Gly (8995)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q64644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment).	3.3E-93	
6825	cg42717162	370	GCCCTATCCATA AACTAGGCCTC G[C/gap]CCCATT CCACTTCTGATT ACCAGAA	C	gap	Ala	Ala (8996)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa.	1.3E-90	
6826	cg42717162	373	CTATCCATAAAA CTAGGCCCTCGCC C[C/gap]ATTCCA CTTCTGATTACC AGAAAGTA	C	gap	Pro	His (8997)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa.	1.3E-90	
6827	cg43248620	2674	CTTTTTTTTGGG AGGAGAAAGGG G[gap]TJTITTTTG GGACAGCTGAA GGCGGCG	gap	T	Pro	Thr (8998)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0	1
6828	cg42175288	1619	GAGGTACGGA GGAGATCGAGG AGG[G/gap]TTAT GGAGGAGATCG AGGAGGCTAT	G	gap	Leu	Tyr (8999)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17

6829	cg42175288	1813	AGGTGGGGACG GAGAGACCGAG GTG[G/gap]CTAT GGAGGCAAAATG GGAGGAAGA	G	gap	Gly	Ala (9000)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17
6830	cg43962927	1470	GGCACTGGCTG GAGAGGGGCTG GGC[C/gap]ACCG GTCCCTGCTGG GGGTCCCAGG	C	gap	Gly	Ala (9001)	FRAMES HIFT	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0	11 (11q13.2)
6831	cg44005808	816	CAACCACAGATG GCACTGCCAACA G[C/gap]AGATGG CCCATACCTTCA AATATTA	C	gap	Ala	Glu (9002)	FRAMES HIFT	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. lpcds:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0	
6832	cg43931615	2554	CAGGTCCTGTTC GGTTGTTTTCCA TT[G/gap]GGAGAC CCAACACTATTA AATCGGA	G	gap	Pro	His (9003)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.3E-227	20
6833	cg43956159	1718	CACCCCTCCTCCT GCCGTGGGGG AG[G/gap]CATCG CCATTTCCCTTG TCACCTGG	G	gap	Ala	Ala (9004)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.4E-159	10

6834	cg43956159	1725	CTCCTGCCGTCG GGGGAGGCATC GC[C/gap]ATTC CCTTGTCACCTG GCTTCCCC	C	gap	Gly	Ala (9005)	FRAMES HIFT	dna_rna_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.4E-159	10
6835	cg43917883	1246	ATCACCAGGGG CCCCCGCCCG GCG[G/gap]GCCC GGCGCCGCAG CGAGGAGAAG	G	gap	Gly	Gly (9006)	FRAMES HIFT	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6836	cg43917883	1247	TCACCAGGGC CCCCCGCCCG CGG[G/gap]CCCG GCGCGCCGAGC GAGGAGAAGA	G	gap	Pro	Pro (9007)	FRAMES HIFT	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6837	cg43917883	1984	GAAAAACAGCAA AGGGAACAAGTT G[A/gap]AAAAAA CATGAAAGATGC AAAAGAC	A	gap	Glu	Glu (9008)	FRAMES HIFT	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6838	cg43917883	1990	AGCAAAGGGAAC AAGTTGAAAAAA A[gap/A]CATGAA AGATGCAAAAGA CAAAATTG	gap	A	Asn	Lys (9009)	FRAMES HIFT	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6839	cg43947431	2147	CCACCAAGGACC GAAGTACCCTGT TIG[gap]GCGATG TCGCCCCCCATC TTATACT	G	gap	Ala	Ala (9010)	FRAMES HIFT	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa.	1.2E-91	
6840	cg43947431	2148	CACCAAGGACC GAAGTACCCTGT TG[G/gap]CGATG TCGCCCCCCATC TTATACTT	G	gap	Ala	Ala (9011)	FRAMES HIFT	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa.	1.2E-91	

6841	cg43940815	436	GAGAAATCTCTCC AGTGTGAGGTTT TTT/gap]ATTGTTG TAAAAAAGAAGA GTTTGG	T	gap	End	End (9012)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	1E-89	6
6842	cg43269833	295	TGTGCTGGGCA GGACGAGGCTG CGG[C/gap]CCCC GGGGGCAGCGT TGGGGCGGGC	C	gap	Pro	(9013)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa.	6.6E-89	13
6843	cg43269833	412	ACCTGTTAGACA CTTCGGACCCTC C[G/gap]GGGGGA GGCGAGACGCG GCTAGTTT	G	gap	Gly	(9014)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa.	6.6E-89	13
6844	cg43299462	971	TGAGGGTGGTCA GCGGCGTCCTG GA[gap/GJCGCCT GGTCTGCCCG GGTCTCTGG	gap	G	Ser	(9015)	FRAMES HIFT	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa. pcls:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.2E-67	3 (2p25)
6845	cg43947402	594	CTTTCATGTTTG GATCAATTTTTT T/gap]GACCCAG CAGGAATGGGT GACACGC	T	gap	Ser	(9016)	FRAMES HIFT	dynein	Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa.	3.7E-214	3
6846	cg43932150	190	CGGACGTGTCG GTGCTGCAGAAG CA[C/gap]CTGCG CAACTGGTGCG GCTGCTGCT	C	gap	Leu	(9017)	FRAMES HIFT	dynein	Human Gene Similar to SWISSPROT- ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	1.1E-89	

6847	cg43958656	2145	TACAAAGCGGAG GACGAGGTGCA GC[G/gap]CGAGA GGGTGTCAGCC AAGAACGCC	G	gap	Arg	Pro (9018)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0	6
6848	cg44017749	14201	CCAGCCAGCCCT TCCCTGGCCCC GC[C/gap]GGATG TATAAATGTAAA ATGAAGG	C	gap	Arg	Gly (9019)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12
6849	cg44017749	5045	CAACACCCAGCC CTTTGACCTGCA G[G/gap]TGTAAC ACCCCTCCCGCC AGCCCAT	G	gap	Val	Cys (9020)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12
6850	cg43950268	1346	AGCTGAGCCAG GCCAGGCTCGC TTG[C/gap]GCGC AGCTGATTACG TTCTTGATG	C	gap	Ala	Gln (9021)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6851	cg43950268	1476	TGCGCAGGAAGT GGCGGGCAGCC CC[C/gap]ATCTC CAGCACGGTGA CCATGGCAG	C	gap	Met	Met (9022)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16



6852	cg43950268	1895	GAGAGGCTGGTT AGCTGCCCCGA GG[G/gap]CAGCG CCGAGGACTCGT AGCGCAGC	G	gap	Pro	Pro (9023)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	18
6853	cg43950268	2239	TTTGGCGGTGTA CAGTGCAACGCT G[G/gap]AGCCCA GCTCCCGGCTCA CATCAA	G	gap	Ser	Ser (9024)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6854	cg43945212	1867	AGAACATTTGCG AACTGGCCCGG AG[G/gap]ATGCT CTTCAGCGCCGT CGAGTGGG	G	gap	Met	Cys (9025)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN AI REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.8E-232	7
6855	cg43985169	659	GCCTCAAAACAAG ATCCTCCAGTTA TT[gap]CATGAA CTTAGAGTATCA CTTGAAG	T	gap	His	Met (9026)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6856	cg43985169	738	AAGATTTCTCGA AAAAGGCTAAAC G[gap]TCTGATG GAAGGAGTTACA GATCTGA	gap	T	Ala	Val (9027)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6857	cg43985169	843	ACTTTTCCAAGA GAAGGAGATGAA A[gap]A/CACCAA ATAGTATTCAG CAGACAT	gap	A	Thr	Asn (9028)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6858	cg43985169	933	AAGGGATGGATC AAATATAATTTAT [A/gap]CTGCTAA AATTAGTTTACG AGAGGC	A	gap	Thr	Leu (9029)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	

6859	cg43985169	968	TAGTTTACGAGA GGCATTGTGTGG C[ <i>gap</i> ]/GJTGCTCA ATTAATGTACCA ACACTGG	gap	G	Cys	Val (9030)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6860	cg43918531	443	TTCACCCCAATCA GAATAGCCGATG G[C <i>gap</i> ]/TATGAG CAGGCTGCTCG CGTTGCTA	C	gap	Tyr	Met (9031)	FRAMES HIFT	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. ipcl:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1E-104	5
6861	cg43949555	1550	CCCTGCTGTAAA GGACATGCTGGA A[G <i>gap</i> ]/CTGGTA TTCTAGATACCTA CCTGGG	G	gap	Ala	Leu (9032)	FRAMES HIFT	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa. ipcl:SWISSPROT-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6862	cg42889246	496	CTCCAGTGGACT CAGCGGCAGAG AC[G <i>gap</i> ]/CCACC CCGAGAAGGCA AATCCACT	G	gap	Pro	His (9033)	FRAMES HIFT	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.5E-73	
6863	cg43972010	2213	ATGCCAGATGGG AGCCTCCCAGAG G[C <i>gap</i> ]/CCAGAG CCTGTGGCCCAAG GCCACTG	C	gap	Ala	Ala (9034)	FRAMES HIFT	esterase	Human Gene SWISSPROT-ID:P17405 SPHINGOMYELIN PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.12) (ACID SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa.	0	11 (11p15.4)

6864	cg43942273	858	TCGGAGAGTGG ATAGCTCATCA CT[G/gap]CATTG GAATCAACCAGC CAAACCTCC	G	gap	Gln	Ser (9035)	FRAMES HIFT	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16
6865	cg43328419	234	TTACCAAGCTAT ACAGCCGACAAG G[C/gap]TACCAC TTGCAGCTGCAG GCGGATG	C	gap	Tyr	Thr (9036)	FRAMES HIFT	tgf	Human Gene Homologous to SWISSPROT-ID:Q92913 FIBROBLAST GROWTH FACTOR-13 (FGF-13) (FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2) (FHF-2) - HOMO SAPIENS (HUMAN), 245 aa.   pcls: SPTREMBL-ID:Q92913 FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2 - HOMO SAPIENS (HUMAN), 245 aa.	2.2E-119	
6866	cg43249494	602	ACAAGGGACAG GAGCGACCAGC ACA[C/gap]AGAC ACCAAATGAGGA ATGTTTGTT	C	gap	Gln	Arg (9037)	FRAMES HIFT	tgf	Human Gene Similar to SWISSPROT- ID:P34004 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 155 aa.	2.3E-61	5 (5q31)
6867	cg43320667	1502	GGTATGCCAGGA ACGCCAGCCCG GG[gap/G]CTGAG GCCGCCACATCA GCAATGGA	gap	G	Pro	Pro (9038)	FRAMES HIFT	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0	3 (3p25)
6868	cg43969076	1807	CACCCACACGAT GGCATAGGAATG G[G/gap]CACTGC CAATCCTCAGCA CCACTCT	G	gap	Ala	Ala (9039)	FRAMES HIFT	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0	7 (7q21.11)

6869	cg43286488	553	CAGGCTGGGCT GGGTAGCACAG GCT[G/gap]GCAC AGCCGCTGGGC AGGGGGCTGG	G	gap	Gln	Ser (9040)	FRAMES HIFT	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. [pdbs:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0	12
6870	cg43065549	1570	GCTGGATGACG CGGCCTGCCTTG CC[C/gap]CAGGG TTATGATGGATG GCAGATTG	C	gap	Gln	Arg (9041)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P18452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6871	cg43065549	1571	CTGGATGACGC GGCCTGCCTTGC CC[C/gap]AGGGT TATGATGGATGG CAGATTCT	C	gap	Gln	Arg (9042)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P18452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6872	cg43065549	2126	CTACAACGGTGT CCTTGCTGCCAA G[C/gap]TCTGGA GGAAGAAAGCTG CACCTCAC	C	gap	Leu	Ser (9043)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P18452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

6873	cg44034764	586	CAGGCGAGGCA GCCCCCAGGCA GTA[ <i>gap</i> /C]AGAG CTGGTAGAAGAT GTGCAACAG	gap	C	Leu	Cys (9044)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6874	cg44034764	586	CAGGCGAGGCA GCCCCCAGGCA GTA[ <i>gap</i> /C]AGAG CTGGTAGAAGAT GTGCAACAG	gap	C	Leu	Cys (9045)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6875	cg43010733	1185	TTCTCTGGACCAC TTCCCGCCCGG CG[G/ <i>gap</i> ]CCGGC AGGACGGCTGG ATCGCCGAC	G	gap	Gly	Ala (9046)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E II) (N- ACETYLGLUCOSAMINYLTRANSFERAS E II) (GNT-II) (GLCNAC-T II) - HOMO SAPIENS (HUMAN), 531 aa.	5E-304	
6876	cg43094362	168	CACTGAGGTGTC AGAAGGCAAAGC C[C/ <i>gap</i> ]ACTGCT CTACTTCATGGT CACCACCT	C	gap	Trp	Trp (9047)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6877	cg43094362	215	CACTCCTGTCCA GGAAGATCAGTG G[C/ <i>gap</i> ]CCCCAC GGTGACATCTGC TTCTTCT	C	gap	Gly	Gly (9048)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7

6878	cg43094362	219	CCTGTCCAGGAA GATCAGTGGCCC C[C/gap]ACGGTG ACATCTGCTTCT TCTGTCA	C	gap	Val	Val (9049)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6879	cg43094362	259	TCTTCTGTCACA TGCCTGCGGTTA C[gap]A]GGGAAG CAGACGTGGAC CACTGGCT	gap	A	Arg	Leu (9050)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6880	cg43924995	1264	TGCAAAATAACAA TCTCAGCTACTG G[G/gap]ATGCCC CCCTGGGAAGTT CTTATAT	G	gap	Asp	Met (9051)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222 X (Xq24)	
6881	cg43924995	330	TGTGCTTCCGCC TCTTCCCGGTTG C[G/gap]GGCTCA GGGCTCGTTCTG GTCTGCC	G	gap	Gly	Ala (9052)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222 X (Xq24)	
6882	cg43987514	339	ACTGGCACATGA GGGGCCCCAGC TG[C/gap]CCCCGA GGCCAAGGCTG CGCTGAACA	C	gap	Gly	Gly (9053)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
6883	cg43987514	544	ACTGGCCAGGTC CACTTGCTGGCC G[C/gap]CTGCTG GCCCGGCTGGT ACGTTTCA	C	gap	Gly	Ala (9054)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	

6884	cg43987514	833	AAGCTGGCCAG GCCAGGTCCAGT CA[G/gap]GGCCC CCAGCCCACCCA GTCCTCCG	G	gap	Leu	End (9055)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
6885	cg43958670	2191	AGGCTTGTAAAGT AGGCCTAGGAC CT[G/gap]AGGCA CTGGACGCTGG AGATTTTGT	G	gap	Ser	End (9056)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.6E-207	1 (1q32)
6886	cg44034752	1095	TGAGAACTTGG TGCGGCAGAGG TT[G/gap]CAGTG ACCTGCACGGTG TTCCAAAC	G	gap	Ala	Gln (9057)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6887	cg44034752	1299	TCCTCCAGGACA CCAGTTGCACCG G[G/gap]CGCACT ACGACCTGCGC CACACCTT	G	gap	Ala	Arg (9058)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6888	cg44034752	1350	CATGGGTGTGGT CTCATTGGGGTC A[G/gap]CCTCAG GAGAAAGTGTCCG ACCCCCG	C	gap	Pro	Pro (9059)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6889	cg43051796	1283	GCCAAAAAAGC AAGGGGAATGA GG[G/gap]TCCCC CCCAGGCATCTG GCACAGCC	G	gap	Thr	Thr (9060)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa. [pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4E-114	3

6890	cg43051796	1301	AATGAGGGGTCCC CCCCAGGCATCT G[G/gap]CACAGC CCCCAGTGCACA TTCTGGG	gap	Ala (9061)	Ala (9061)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.lpcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4E-114	3
6891	cg43924574	1299	TCTCAGGGGTGA ATTTCTCTGGTT C[C/gap]TGCCGG TCCTGGGACCAG TTGGTAA	gap	Gln (9062)	Gln	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1E-106	1
6892	cg43255952	678	AGAGGGCGGGTG CACGGGTACTGT TC[C/gap]TCACG GCAGTCAAGAG GCCCCAGGCT	gap	Glu (9063)	Glu	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
6893	cg43255952	935	TCATACTGGCCC TGAGCCAGCAAG C[C/gap]TGCAGG CAGGAATAGCAG GAAGAGG	gap	Ala (9064)	Gly	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)



6894	cg43967180	92	GGGGACCTGCC CTCCTGGACGC GGA[G/gap]CCTA AACCTGAGTTAC AACAAACTC	G	gap	Ser	Thr (9065)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P70193 MEMBRANE GLYCOPROTEIN - MUS MUSCULUS (MOUSE), 1091 aa.	1.7E-99	
6895	cg43917300	269	TGAGGGCCACC ACCCCACTGTGG GG[G/gap]CTCAC CTTCGGGTGGT GAAAAAGC	G	gap	Ser	Ser (9066)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	4.4E-99	22 (22q13.3 )
6896	cg43917300	527	TCTCAGGGCACT CGAAGGCCAGG CA[G/gap]CGGAA GCCGCCCTGGA TGTTGAAGC	G	gap	Arg	Arg (9067)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	4.4E-99	22 (22q13.3 )
6897	cg43252493	320	AATGTAATGCCA CCAACGCCATTG G[C/gap]TCCGCC TCTGTTGTCACT GTCCTCA	C	gap	Ser	Pro (9068)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	1.8E-84	
6898	cg43252493	326	ATGCCACCAACG CCATTGGCTCCG C[C/gap]TCTGTT GTCACGTGCTCTC AGGGTGC	C	gap	Ser	Leu (9069)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	1.8E-84	

6899	cg43512398	91	TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA	C	gap	Lys	Ser (9070)	FRAMES HIFT	glycoprotein	Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	2.7E-83	17 (17q23)
6900	cg44341920	91	TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA	C	gap	Lys	Ser (9071)	FRAMES HIFT	glycoprotein	Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	2.7E-83	17 (17q23)
6901	cg43983795	1467	TGCTTCCTTATC CAGGCAAAATGT G[G/gap]CAAGGC CCCTGGATGCAT CTCTTCC	G	gap	Ala	Ala (9072)	FRAMES HIFT	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.2E-74	X

6902	cg43056971	238	CAATCCGTCAGC TAAACCCAGTGT G[T/gap]GGCTGA GATCCAAAATTG GGACAGT	T	gap	Trp	Gly (9073)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2 - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa.	2.2E-72	1
6903	cg43995037	2835	GGCTCAGGAAC T GCGTGCGGGCG TA[G/gap]CGGGT GAGCATGCTGAT GATGACCA	G	gap	Arg	Arg (9074)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TAURUS, 937 aa. ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TAURUS, 937 aa.	3E-68	15
6904	cg42887075	230	CGGGTGAAGAA GTCAGGGCCTC GGC[C/gap]ACAG GGCCCCAGGGA AAAGGAGGCC	C	gap	Pro	His (9075)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	1.3E-58	
6905	cg43926142	652	TTTAATTAAGAA TGAGTGCTGGG G[C/gap]CCITTTT ATTGGGTACTGC ATCTAC	C	gap	Ala	Ala (9076)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q15388 MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL 20 KD OUTER MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20) (KIAA0016) - HOMO SAPIENS (HUMAN), 145 aa.	2.9E-57	1

6906	cg43250682	1070	GCCAAAGAAGCA GGAAAAAGGGG CAG[G/gap]CTTG AGGACGCCTCCA TTCTATGCC	G	gap	Leu	Leu (9077)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6907	cg43250682	1483	TTTCAAGGAAAG CCTAATTTTGAA G[A/gap]ATACTTT GAAATTCTGACT CCAAAA	A	gap	Glu	Asp (9078)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6908	cg43250682	1484	TTCAAGGAAAGC CTAATTTTGAA A[A/gap]TACTTTG AAATTCTGACTC CAAAAA	A	gap	Tyr	Thr (9079)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6909	cg43250682	2104	GATGTCTACAAG GTGGAGACCAAT G[G/gap]CGATGC CTATTGTGTGGC TGGGGGA	G	gap	Gly	Ala (9080)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6910	cg43250682	2123	CATTGGCGATGC CTATTGTGTGGC T[Gap/T]GGGGGA TTACACAAAAGAG AGTGATA	gap	T	Gly	Trp (9081)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6911	cg43250682	2551	TTCCAAAAGAAA GATGTGGAAGAT G[G/gap]CAATGC CAATTTTTTAGG CAAAGCA	G	gap	Gly	Ala (9082)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6912	cg43250682	2555	AAAAGAAAGATG TGGAAGATGGCA A[T/gap]GCCAAT TTTTTAGGCAAA GCATCAG	T	gap	Ala	Pro (9083)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4

6913	cg43250682	2574	TGGCAATGCCAA TTTTTAGGCAA A[G/gap]CATCAG GAATAGATTAGC AACCTAT	G	gap	Ala	His (9084)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6914	cg43956596	2876	AACCCAGCGGTCA GGCGGAGCCGG CA[G/gap]GACGG GCCCAGGTCAGT GTTTCAGG	G	gap	Arg	Arg (9085)	FRAMES HIFT	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
6915	cg43919913	1197	GGTCGATCAGTG TCCGGTAACCCT C[C/gap]TGCGGG TCTTCTTGGA GCATTAC	C	gap	Gln	Gln (9086)	FRAMES HIFT	helicase	Human Gene SWISSNEW-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa.lpcis:SWISSPROT-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa.lpcis:SPTREMBL-ID:Q14562 PUTATIVE RNA HELICASE HRH1 - HOMO SAPIENS (HUMAN), 1220 aa (fragment).	0	17
6916	cg44026400	245	TCGCCCTATTTC TTC TTGGCGGCC G[C/gap]CTTCTT AGGCTTGACAAC CTTGGGC	C	gap	Ala	Arg (9087)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6917	cg44026400	246	TCGCCCTATTTC TCTTGGCGGCC GC[C/gap]TTCCTT AGGCTTGACAAC CTTGGGCT	C	gap	Lys	Lys (9088)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6

6918	cg44026400	282	TGACAACCTTGG GCTTAGCGCCT TG[gap]GGCTTC ACAGCCTTAGCA GCACTTT	G	gap	Pro (9089)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6919	cg44026400	356	ACCTTGGCCTTC TTTGGGCTCTTA G[C/gap]CACTTT CTTGGTTACAGT GGCCGCG	C	gap	Ala (9090)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6920	cg44026400	357	CCTTGGCCTTCT TTGGGCTCTTAG C[C/gap]ACTTCT TGGTTACAGTGG CCGCGG	C	gap	Val (9091)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6921	cg44026400	383	ACTTCTTGGTT ACAGTGGCCGC GG[C/gap]CGGCT TCTTCGCTTCTT CGGTGTT	C	gap	Pro (9092)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6922	cg44026400	384	CTTCTTGGTTA CAGTGGCCGCG GC[C/gap]GGCTT CTTCGCTTCTT CGGTGTT	C	gap	Pro (9093)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6923	cg44026400	532	AACCTTGGGCTT GGCTTCCCCGG AG[G/gap]CTGCC TTCITGTTGAGT TTAAAGGA	G	gap	Ala (9094)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6924	cg44026400	720	AAACTCCGCTAC GCTCTTTAGAGG C[G/gap]GCCACA GCCTTGGTGATG AGCTCTG	G	gap	Ala (9095)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6

6925	cg42689683	363	CCAGCTCCAGGA CCTTGGCCGTCA G[G/gap]TACTCA ATAACCGCAGCG AGGTAGA	G	gap	Tyr (9096)	Tyr (9096)	FRAMES HIFT	histone	Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa.	3.7E-53	
6926	cg42689683	519	CCGCCCCCGGC CGCCAGCACCG GAG[gap]GACCC TCGGCGTCTCCT CCTCCTCGG	gap	G	Ser (9097)	Ser (9097)	FRAMES HIFT	histone	Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa.	3.7E-53	
6927	cg43985818	429	AGACGCCGTCAC CTATACGGAGCA C[G/gap]CCAAGC GCAAAACTGTCA CAGCCAT	G	gap	Ala (9098)	Pro (9098)	FRAMES HIFT	histone	Human Gene Similar to TREMBLNEW- ID:G2564108 HISTONE H4 - CHAEPTERUS VARIOPELATUS, 103 aa.pcls:TREMBLNEW-ID:E314007 HISTONE H4 - MUS MUSCULUS (MOUSE), 103 aa.pcls:TREMBLNEW- ID:G62736 H4 HISTONE - CAIRINA MOSCHATA (MUSCOVY DUCK), 103 aa.pcls:TREMBLNEW-ID:G1493809 HISTONE H4-VI - GALLUS GALLUS (CHICKEN), 103 aa	4E-50	
6928	cg43988803	464	CTGCCCCCGGC GCGCTCGTGCA CCT[G/gap]GCCG CTGCCACAGGC GGAGTTTAGC	G	gap	Trp (9099)	Cys (9099)	FRAMES HIFT	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1 )	13
6929	cg43332152	1175	CAGCTGAGCGC CCTGGCGGCC GGC[G/gap]CCAC GCCTCTTCCGC AGTCCGCGC	G	gap	Arg (9100)	Pro (9100)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17

6930	cg41637704	1220	GCGCCGCGGAGA CAAGGGCAGCG GAC[gap/C]CGCC TGCGGACTTGAG GGACAGTGA	gap	C	Pro	Pro (9101)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7
6931	cg43983917	1204	CCCGGTGCGGA TCTGGCGGCCTA CA[C/gap]ACGCT GCGCTAAGCTGC AACGAAAA	C gap	Thr	Asn (9102)	Asn (9102)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.3E-216	
6932	cg43143467	406	GCAGAACAGCTG GAGGAACCTGGA GC[A/gap]CGTTG CTTTTGAGAGAA CTCATTAC	A gap	His	Pro (9103)	Pro (9103)	FRAMES HIFT	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6933	cg42908326	783	TGTGGCGCACG CGCACCAACCACC TG[C/gap]ATCCG CACCTGGCCGC GCACGCGCC	C gap	His	Ile (9104)	Ile (9104)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
6934	cg42908326	833	CCTACATGATGT TCCCAGCACCCGC C[C/gap]TTCGGA CTGCCGCTCGC CACGCTGG	C gap	Phe	Ser (9105)	Ser (9105)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
6935	cg42489148	1154	CACCACAGCCG CCTCCGCCGCC ACC[C/gap]ACAG CCTCCCCAGCCT CAGCCAGGT	C gap	Pro	His (9106)	His (9106)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6E-118	13



6936	cg42489148	872	GGAACCTGTGC GAGTGGATGCG GAA[gap/G]CCGG CGCAGCAGTCC CTCGGCAGCC	gap	G	Asn	Lys (9107)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6E-118	13
6937	cg43983244	2275	TGGTGAGTCCCG GCGACTCCAGCA G[G/gap]CTCCGG CCAGCCTCGCC CACGTTCT	gap	G	Ser	Ser (9108)	FRAMES HIFT	homeobo x	Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEBOX PROTEIN 1 (HOMEBOX PROTEIN MHOM) (HOMEBOX PROTEIN K-2) (RHOM) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa.	2.2E-113	
6938	cg43932912	729	TGACAGCAAGTC CATTAGCTCAA G[G/gap]CAGAAC TGCCTTAAATGT TCATACT	gap	G	Cys	Cys (9109)	FRAMES HIFT	homeobo x	Human Gene Similar to SWISSPROT- ID:P34349 HYPOTHETICAL 30.5 KD PROTEIN C30A5.3 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 261 aa.	1.3E-81	
6939	cg43988195	3178	TGTCAAATACCA GGAGGGCATCA GC[C/gap]GCAAA CTCCTCTGAGCT GGTGTACC	gap	C	Ala	Ala (9110)	FRAMES HIFT	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.6E-53	12
6940	cg42503642	2466	ATGCCAATGCAA ACATTATTCTGA [G/gap]GCCAAGC CCGAAGGACCTA GAGTCA	gap	G	Ala	Pro (9111)	FRAMES HIFT	hydrolas e	Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa.	0	

6941	cg42503642	2467	TGCCAATGCAAA CATTATTTCTGA G[G/gap]CCAAGC CCGAAGGACCTA GAGTCAA	G	gap	Ala	Pro (9112)	FRAMES HIFT	hydrolase	Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa.	0	
6942	cg43296921	405	TGGAGCCGAAGT TTTCTGGCTCCG G[C/gap]CCGCTG ATGGTCCAGAA GCCAGGA	C	gap	Gly	Gly (9113)	FRAMES HIFT	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	15 (15q23)	3.3E-238
6943	cg43933380	1392	ACATGTAAGACT CCTTCTGCTGAA A[C/gap]ACAGTA CTGAGAAATTCAG TGAGGAT	C	gap	Val	Phe (9114)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	6	1.4E-261
6944	cg43933380	300	ACCTAGGAACCA GGAGTACTGGAT A[C/gap]TGTTCC GTTACTGGTAAC CTATCTG	C	gap	Gln	His (9115)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	6	1.4E-261
6945	cg43933380	349	TGGATGTAAAGG TTCATAAGTTAC A[A/gap]TGCTTTT TTTGTTTAAAAA AAAAA	A	gap	Ile	Met (9116)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	6	1.4E-261
6946	cg43933380	374	ATGCTTTTTTGT TTAAAAA A/gap]AAAGTCTG TACTTTACAAGC CAAAA	A	gap	Phe	Phe (9117)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	6	1.4E-261

6947	cg43933380	377	CTTTTTTTGTTTA AAAAAAAAAAAAAA[ A/gap]GTCGTAC TTTACAAGCCAA AAGTG	A	gap	Phe (9118)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
6948	cg43931810	819	GAACACAGAGGG CATAGCGTGGTG AG[C/gap]GTCCG CTTCCTCCGTG AAGGTAAT	C	gap	Arg (9119)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa.	1.2E-240	19
6949	cg43956260	570	AGTGTTACCTGG AACTTCGGTGGG G[G/gap]GCCCAG GCCCTGAAAGTA CCTGACC	G	gap	Pro (9120)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
6950	cg43956260	571	GTGTTACCTGGA ACTTCGGTGGG GG[G/gap]CCCAG GCCCTGAAAGTA CCTGACCA	G	gap	Gly (9121)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
6951	cg43926568	1529	CTCTTCAGGGCT TCCTCATTCTGG C[C/gap]TTTCAG GTGTTTCACATA GGCTAGT	C	gap	Ala (9122)	FRAMES HIFT	interferon	Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa.	4.8E-141	10 (10p23)

6952	cg43922672	1616	GGGACCACGCA CCATGATGCCTT GG[C/gap]CATCC TCCGCCAAGCTC GAGAGCCC	C	gap	Ala	Ala (9123)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6953	cg43922672	1687	AAGGAAGCTGAC TCCAGAGGCCAT G[C/gap]CCGACC TCAACTCCTCCA CTGACTC	C	gap	Pro	Pro (9124)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6954	cg43922672	1760	AGTGATGTTTCT GTAGAATCTACA G[C/gap]AGAGGC CACAGTCTGCAC GGTGACA	C	gap	Ala	Glu (9125)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6955	cg43930054	1773	CGATCTGGGCCA GTGGATCACTGC T[G/gap]GCCAAC AGCCGCGCCAC TTCGCTGT	G	gap	Ala	Ala (9126)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
6956	cg43930054	1818	CGCTGTTGGAAC CCATCTTCCCCC A[G/gap]GCATAC TGCTGCACCGCA CAGGAAA	G	gap	Ala	Ala (9127)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
6957	cg43930054	633	AGCAGGCACGG AATATCAGCAGG TC[C/gap]TTCGG CTCAGTAAGCTT CAGTGAGA	C	gap	Lys	Lys (9128)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)

6958	cg43297395	1744	GCGCCCCAGCT GCCTCTGGCTGT GG[C/gap]CACAG ACAACTTCATCA GCACCTGT	C	gap	Ala	Ala (9129)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:Q15589 TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 626 aa.	0	9
6959	cg43259301	1495	GCCCCATCCCCA TCCACACAAGTA C[A/gap]GCGCAG CGTGTCGGCCAA TCCCAAG	A	gap	Gln	Arg (9130)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q15524 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 745 aa.	0	13
6960	cg43299934	1634	TGACCACAATGA CCTCCACGGTGA T[G/gap]CCATCA GGCAGCATGAG CCAGGATG	G	gap	Gly	Gly (9131)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 903 aa.	0	17
6961	cg43336163	2426	CTTCCCCTCTAG ATGGCCCCCCG GC[C/gap]GTGGC TGTGGGCCAGT GCCCGCTGG	C	gap	Val	Trp (9132)	FRAMES HIFT	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA IJ} - HOMO SAPIENS, 616 aa.	0	19
6962	cg43336163	2464	CAGTGCCCGCT GGTGGGGCCAG GCC[C/gap]CATG CACC GCCGCA CCTGCTGCTC	C	gap	Pro	Pro (9133)	FRAMES HIFT	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA IJ} - HOMO SAPIENS, 616 aa.	0	19
6963	cg43336163	2465	AGTGCCCGCTG GTGGGGCCAGG CCC[C/gap]ATGC ACCGCCGCCAC CTGCTGCTCC	C	gap	Met	Cys (9134)	FRAMES HIFT	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA IJ} - HOMO SAPIENS, 616 aa.	0	19

6964	cg43336163	944	CCGACTTCTTGC AGTGGCGGAG CC[C/gap]ATCGT GGTGAGGCTTAA GGAGGTCC	C	gap	Ile	Ser (9135)	FRAMES HIFT	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
6965	cg44929725	2841	AAGAGCAGAATC CAGATATTGTTT C[gap/C]AGAAAA AAACCAGCAAC TGAAGTG	gap	C	Ser	Ser (9136)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6966	cg44929725	2851	TCCAGATATTGT TTCAGAAAAAA A[gap/A]CCAGCA ACTGAAGTGAC CCCACAC	gap	A	Pro	Thr (9137)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6967	cg44929725	2856	ATATTGTTTCAG AAAAAAACCAG C[gap/C]AACTGA AGTGGACCCAC ACATTTT	gap	C	Ala	Ala (9138)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6968	cg44929725	2864	GAGCTCTGCAG GTATGACCCCGA AG[G/gap]GGACA ATACAGGGGAG CAGGTGGCT	G	gap	Gly	Gly (9139)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6969	cg44929725	2865	AGCTCTGCAGGT ATGACCCCGAAG G[G/gap]GACAAT ACAGGGGAGCA GGTGGCTG	G	gap	Asp	Thr (9140)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6970	cg44929725	2866	GCTCTGCAGGTA TGACCCCGAAG GG[G/gap]ACAAT ACAGGGGAGCA GGTGGCTGT	G	gap	Asp	Thr (9141)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)

6971	cg43988890	150	GACATGGAGCC CGAGCGCGCG CCG[G/gap]CGCC GGCCCGCGGCC TCTTCGGCTG	G	gap	Arg	Ala (9142)	FRAMES HIFT	kinase	Human Gene SWISSNEW-ID:P15056 B- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa.   pcis:SWISSPROT-ID:P15056 B-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa.	0	7 (7q34)
6972	cg43257904	505	GGCGGGGCGCT AAGGCACAAGG CGG[G/gap]CTGC GCTGAGTAGGCA GGCAGGGCAA	G	gap	Ala	Ala (9143)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0	X (Xp11.4)
6973	cg43257904	807	TGTAAGGCAGTG AGCCAGTCATAA G[C/gap]TCGTAG AGCACAAACCCCG TAGGCAT	C	gap	Glu	Asp (9144)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0	X (Xp11.4)
6974	cg43016269	1920	GCAAAGGAGCTA GAAGAGGAGATT A[C/gap]CTTACG GAAAAGTGTGGA ATCAGCA	C	gap	Thr	Thr (9145)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa.	0	
6975	cg43263359	1179	AGATGGGGCCC CGCAGCGCGCG AGA[G/gap]CTCG GCAAAGTCGTCCA CCTCGTCCT	G	gap	Ser	Ser (9146)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment).	0	
6976	cg43263359	1239	CTGCCCTCTGACT TGCCAGCCTCTG G[C/gap]TCCTCA GCCTCCGCTTCG TGAGCTT	C	gap	Glu	Asp (9147)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment).	0	

6977	cg43947749	1457	CTCATCCCTCCT CACTTGAGGTCC C[C/gap]AGCGGG CACTACCACCCT CACCCCG	C	gap	Pro	Gln (9148)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6978	cg43947749	1457	TCATCCCTCCTC ACTTGAGGTCCC C[gap/C]AGCGGG CACTACCACCCT CACCCCG	gap	C	Pro	Pro (9149)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6979	cg43947749	1461	TCCCTCCTCACT TGAGGTCCCCAG C[G/gap]GGCACT ACCACCCCTCACC CCGTCCT	G	gap	Gly	Ala (9150)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6980	cg43947749	1463	CCTCCTCACTTG AGGTCCCCAGC GG[G/gap]CACTA CCACCCCTCACCC CGTCCCTCA	G	gap	Gly	Ala (9151)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6981	cg43947829	910	TGTTCAAGTACT TCTCTGAGCATT G[G/gap]CCTCTG GCTGGGATTATG CTTCAAC	G	gap	Pro	Gln (9152)	FRAMES HIFT	kinase	Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
6982	cg38438124	1248	GAGAGCGATGG CACCCACCGGT GG[G/gap]AACCC CCCCAGATAGCC CCGGGAAT	G	gap	Gly	Glu (9153)	FRAMES HIFT	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KI-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.8E-216	10



6983	cg43917871	1455	ATTGGGGCTGCT GACGGGCGTAC TG[C/gap]CCCCCT GGCATGCTAGAT GAACCCAT	C	gap	Gly	Ala (9154)	FRAMES HIFT	kinase	Human Gene S'WISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
6984	cg44131752	1284	TGCCCCCTGCCCA CCAGGTAAGG GG[G/gap]CCTGT GGCAGCAAGATA GGGGGAGA	G	gap	Pro	Leu (9155)	FRAMES HIFT	kinase	Human Gene S'PTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.8E-173	16
6985	cg44000392	347	CGGCATGGAGA AGGACGGCCTG TGC[gap]C/GCGC TGACCAGCAGTA CGAATGCCGT	gap	C	Arg	Pro (9156)	FRAMES HIFT	kinase	Human Gene S'WISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
6986	cg43257282	1015	ATGGCTGTCGGA GGCCGGGCTGC GC[C/gap]TGCTG CACTTCCTGTTC ATGTACGA	C	gap	Leu	Cys (9157)	FRAMES HIFT	kinase	Human Gene Homologous to S'PTREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa.	2.8E-147	18
6987	cg44016530	578	TGTAGTCTCTTT GGTGATCTCATC T[G/gap]CTTTTCT GCTCGAGTGATG ACAGCC	G	gap	Ala	Glu (9158)	FRAMES HIFT	kinase	Human Gene Homologous to S'PTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12
6988	cg44016530	583	TCTCTTTGGTGA TCTCATCTGCTT TT[gap]CTGCTC GAGTGATGACAG CCTTGAA	T	gap	Arg	Arg (9159)	FRAMES HIFT	kinase	Human Gene Homologous to S'PTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12
6989	cg43022553	502	TGCTGGGGCTG AGAGAGGGCTG CAA[G/gap]CTGC TCGTGCACGGCT TTGAGCTGC	G	gap	Leu	Leu (9160)	FRAMES HIFT	kinase	Human Gene Homologous to S'PTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa.	1E-102	

6990	cg43022553	754	CATCCTGGAGCT TGCGGGCCCATG GC[C/gap]ACCCAC CTCATGGTCAGG AGGGTTGT	C	gap	Val	Val (9161)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa.	1E-102	
6991	cg43952004	2215	GCAGAGGAAATC AAACCCCTGCTT G[G/gap]CCACAG CCCCTAGTGTGT CAGCTAT	G	gap	Ala	Ala (9162)	FRAMES HIFT	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.3E-94	14
6992	cg43966625	270	TTCACCTTCCTC AGGCAGGAGCT GC[C/gap]TGTGC GCCTGGCCCAACA TCATGAAA	C	gap	Pro	Leu (9163)	FRAMES HIFT	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. [pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-89	17
6993	cg43917718	694	AAAGGTGGGT GGAATGCTGGCT CG[G/gap]CCCTG CCAGTCACTGGG TGGCAGCA	G	gap	Pro	Arg (9164)	FRAMES HIFT	kinase	Human Gene Similar to SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	1.4E-79	17
6994	cg41501665	381	GCCAAGGCGC GCTGCTGGGA CCA[G/gap]CGGC CTCAAGCGCCG CTTCAGCCGC	G	gap	Ser	Thr (9165)	FRAMES HIFT	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.7E-76	
6995	cg43923082	257	AGGAGACGGGT GCTTTGGCTGCG GC[C/gap]AAAGT CATTGAAACCAA GAGTGAGG	C	gap	Lys	Lys (9166)	FRAMES HIFT	kinase	Human Gene Similar to SPTREMBL- ID:O08815 PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 1206 aa.	9.4E-58	

6996	cg44021449	3311	TTGCTGCTGCAG CAAGGGCTACTG C[C/gap]ACACAG TAGCTGTTAGCC CACAGGC	C	gap	Pro	His (9167)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0	15
6997	cg43322545	1486	GTACCCCTGGAG GCCTGGCGCCC AG[G/gap]GGAAG CACAGCCAGTCC ACCAGCTG	G	gap	Gly	Gly (9168)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.pcds:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
6998	cg43322545	1487	TACCCCTGGAGG CCTGGCGCCCA GG[G/gap]GAAGC ACAGCCAGTCCA CCAGCTGG	G	gap	Glu	Lys (9169)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.pcds:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
6999	cg43991478	544	CACAGGGACATT TGTCGGGCCGT GG[C/gap]AGCCT CTCCCCCTCGTTC CAGCAACT	C	gap	Leu	Leu (9170)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	

7000	cg43998555	1379	GGTCCGCGCCT GGCTGGAAGCC AAG[G/gap]CCTT CAGCCCGCGGA TCGTGGAGAA	G	gap	Ala	Pro (9171)	FRAMES HIFT	kinaserec eptor	Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa  pcis:SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa	1.2E-99	11
7001	cg43942537	2552	TTCTTAATTGTTT TGCCCTTTGGC [C/gap]AAATAAG AGGTAGATTCTT GTTTCA	C	gap	Gly	Ala (9172)	FRAMES HIFT	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa  pcis:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa	0	10
7002	cg43987378	830	GAGCTGGAAGA GCGGCTGAGCA CGC[gap]CJAGGA GGCTTGGTGC AAGAGCTTCA	gap	C	Gln	Pro (9173)	FRAMES HIFT	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.5E-254	6
7003	cg43987378	931	TAGAGGAGAAG GAGAGGAGGCT GCA[G/gap]ACAT CAGAAAGCAGCC CTGTCAAGCA	G	gap	Thr	His (9174)	FRAMES HIFT	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.5E-254	6
7004	cg43953676	552	CTGTGTGCAGAC CGGGGTGACCG GG[G/gap]JTCACC AAGTCTGTAC CTGTGCGA	G	gap	Val	Ser (9175)	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P11047 LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN) - HOMO SAPIENS (HUMAN), 1609 aa.	0	1 (1q31)

7005	cg43983535	1209	CTGTTGCAAAAT CAGCATGATTGA T[G/gap]CGAGCC ATGTAAAAAGC AAGCCGG	G	gap	Arg (9176)	Arg	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7006	cg43983535	338	GCAAAATTAAACC TCCAGTGGCTTG C[C/gap]TGTGCC TTTGGTGAGCTT CAGGGAT	C	gap	Gln (9177)	Gln	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7007	cg43983535	722	GAAGAACTCCAG TCGTTGTAGTTG T[gap/C]GCGGAA TTCAAATTCTACA AGAAGG	gap	C	Thr (9178)	Thr	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7008	cg43983535	726	GAAGTCCAGTCG TTGTAGTTGTGC G[G/gap]AATTCA AATTCTACAAGA AGGTCCA	G	gap	Phe (9179)	Phe	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7009	cg43296393	1540	GGCCTACCTGG CTGCCCTCACCC AG[gap/C]TCCGC GCTCTGGTCTAC TACGCCCA	gap	C	Ala (9180)	Val	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	
7010	cg43296393	1620	TACTCTTCTTTGA GGGCGACGAGG G[G/gap]CTCACC GCCGACTTCCTC CGGGAGT	G	gap	Ser (9181)	Leu	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	
7011	cg43296393	1636	CGACGAGGGGC TCACCGCCGACT TC[C/gap]TCCGG GAGTATGTCACG CTGCATAA	C	gap	Ser (9182)	Leu	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	

7012	cg43296393	2183	AACGGAGCCTG GAGCTGTGGCC GCG[ <i>gap</i> ]CCCC AGCAGGCACCC CGCTCGCGGT	<i>gap</i>	C	Arg	Arg (9183)	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	0
7013	cg43921881	455	GGGGAGCTGG ACCTGGCGGG GAG[C/ <i>gap</i> ]CCCC TCAGCTGAGGAC TCGACATTG	C	<i>gap</i>	Ala	Leu (9184)	FRAMES HIFT	MHC	Human Gene Similar to SWISSPROT- ID:P46378 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	2.6E-63	14
7014	cg43921881	512	GACGGAGCCAC GGATGAGGCCT GCC[C/ <i>gap</i> ]AGGA CCAGGGGAAG GTGGCCTCTG	C	<i>gap</i>	Gly	Gly (9185)	FRAMES HIFT	MHC	Human Gene Similar to SWISSPROT- ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	2.6E-63	14
7015	cg43957213	580	GTGGGGTTTCCC ACCCAAGTTCAA G[ <i>gap</i> ]/GJAGGAGG AGCAGACATCTG TGCTACT	<i>gap</i>	G	Leu	Pro (9186)	FRAMES HIFT	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. pcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. pcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa.	0	1 (1p36.1)

7016	cg43924981	481	CCACCGCGTGC CCTTCCACCGTG TG[G/gap]ACACC ATCTCCGTCAAT GGCTCTGT	G	gap	Asp	Thr (9187)	FRAMES HIFT	misc_cha nnel	Human Gene Homologous to SPTREMBL-ID:P97840 URATE TRANSPORTER/CHANNEL - RATTUS NORVEGICUS (RAT), 322 aa.	2.4E-130	
7017	cg43309398	825	TGGAGAAATGGGA GATTGTGAGTGC A[gap/A]CAGGGA GCAAAGGAAACA GAACCGA	gap	A	Gln	Thr (9188)	FRAMES HIFT	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.1E-67	15 (15q24)
7018	cg43991048	6715	TTGCGAGGGTC GAGCAATTTGCT GG[G/gap]TTTCT GCCTCTGCGTTT CCCATAAAT	G	gap	Thr	Thr (9189)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0	17
7019	cg30421838	2225	CTGGAGGAGGA GCCGCGGCTTG TCC[C/gap]GCCG GGGCGGCAGC AGGAGGCGTC	C	gap	Ala	Pro (9190)	FRAMES HIFT	nuc_rec pt	Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. pcis:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
7020	cg43249083	2410	CAAGCTGCTGCT CAAGCTGCCGG AC[C/gap]TGCGG ACCTGAACAAC ATGCATTG	C	gap	Leu	Cys (9191)	FRAMES HIFT	nuc_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
7021	cg43949686	1962	TATGACATGATG GAGGGCCCGCT GG[G/gap]CAGAG CCATCTCCTCAG CCAGCATC	G	gap	Gly	Ala (9192)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	

7022	cg43949686	2149	GGGAGGCCAAG CTCCTAAAGCGG GA[G/gap]GGCAC GCCTCCGCCCC CACCGCCCT	G	gap	Gly	Ala (9193)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7023	cg43949686	2207	CCTGACCGAGG CCTACAAGACGC AG[G/gap]CCCTG GGCCCCCTGAA GCTGAAGCC	G	gap	Ala	Pro (9194)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7024	cg43949686	2308	ATGAGATCCCGC GCGAGGAGCTG CG[G/gap]CACAC GCCCCGAGCTGC CCCTGGCCCC	G	gap	His	Thr (9195)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7025	cg44128653	1705	ATGAGTGCCCTG CCGTCCCGCCA GC[C/gap]TCCGG AGCTCTCGTCCA GATACTTG	C	gap	Gly	Ala (9196)	FRAMES HIFT	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.pcls:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.4E-203	19
7026	cg43947341	295	GCTCTTACTTTC TGAGGGCCCCAG GC[C/gap]TGGGC ATAAGGCCAGAT CTTCTCTT	C	gap	Gly	Ala (9197)	FRAMES HIFT	nuclease	Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa.	1.1E-115	



7027	cg43969123	2515	CATCGGCAAGAA CCACGTGGCAGT G[C/gap]CCACAC ACTTCTTCAAGG TGCTGAT	C	gap	Pro	Pro (9198)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa.	1.2E-65	9
7028	cg43969123	2517	TCGGCAAGAACC ACGTGGCAGTG CC[C/gap]ACACA CTTCTTCAAGGT GCTGATCC	C	gap	Thr	His (9199)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa.	1.2E-65	9
7029	cg43242829	570	GCGTGCTCAGCT GGCTTCGTGGAC G[G/gap]CACAGC CCTGGCGGACC TCAGCCAT	G	gap	Gly	Ala (9200)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:Q17533 RIBONUCLEASE PH-LIKE PROTEIN B0564.1 - CAENORHABDITIS ELEGANS, 312 aa.	2E-50	
7030	cg43951535	1528	ATCTGGTGGTGA ACTACAGCGAGT A[G/gap]CTTTTA GCCCTTTGCTTG GGCAAAC	G	gap	Ala	Leu (9201)	FRAMES HIFT	nuclease nhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)
7031	cg43918816	581	GGGACCCCATC CCCATCTCGAGG AG[G/gap]CCCCG CCCATTTGTCTT CCTCCGCC	G	gap	Pro	Leu (9202)	FRAMES HIFT	oncogen e	Human Gene SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	0	19
7032	cg44012756	5289	TGCTGCTGTCCC GCAAGCGCCGG CG[G/gap]CAGCA TGCCACAGCTCTG GTTCCCTG	G	gap	Gln	Ser (9203)	FRAMES HIFT	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
7033	cg42732993	592	CAC TGGATTAA GCAGAGTTCAAA A[G/gap]CCCTTC AGCGCCAGTA GCATCTGA	G	gap	Ala	Pro (9204)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN - HOMO SAPIENS (HUMAN), 284 aa (fragment).	6E-150	

7034	cg43918770	4789	AGAGGATCTGGAG CAGCCAAGGAG AC[G/gap]GCAGC AGCCAGCCTGAT ACGATTTC	gap	Gly	Ala (9205)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7035	cg43918770	4790	GAGGATCTGGAC AGCCAAGGAGA CG[G/gap]CAGCA GCCAGCCTGATA CGATTTC	gap	Gly	Ala (9206)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7036	cg43918770	4821	GCCAGCCTGATA CGATTTCATCG C[C/gap]TCACGG ACGCTCTCAGAAC ACGCTGG	gap	Ser	His (9207)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7037	cg43297056	986	AGACTTCGGAC TTTCTTGATGGG G[gap/C]TCCGCC GCAGCCCAGGC TTCCTCTT	gap	Thr	Ser (9208)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103 (20q13.1)	20
7038	cg43292762	1145	AGACTACTGTAT CAGGGACCCGAG AG[G/gap]CAGGC TCCCTGGGTACA GCAGGCCG	gap	Ala	Gln (9209)	FRAMES HIFT	oncogen e	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3E-84 7 (7q31)	15
7039	cg43307658	1767	AGACTTCTCC CAACCGGCCAC GC[C/gap]ACACC TGGGAGTGGCA CAGCTGCCA	gap	His	Thr (9210)	FRAMES HIFT	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15

7040	cg43307658	1853	ACGACCTACTGG ATGCAGCCACAG G[C/gap]AAGAAG GTGCCGAGGG CCACAAGG	C	gap	Lys	Arg (9211)	FRAMES HIFT	oxidase	Human Gene SPTREMBL-ID:Q8397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15
7041	cg44028217	584	CCATGGAGTAGA TCTGCAGGCGGT A[gap/G]CTGCCG TTGTGGCCCCAG GGGTTCT	gap	G	Tyr	Leu (9212)	FRAMES HIFT	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0	7 (7q31)
7042	cg43969851	1187	CAGAGGCCAC ATCTCCAGCTGC AA[G/gap]CTGGG CCCCCAGGTGTC ACTGGACC	G	gap	Leu	Trp (9213)	FRAMES HIFT	oxidase	Human Gene TREMBLNEW- ID:G1890108 LYSYL OXIDASE- RELATED PROTEIN - HOMO SAPIENS (HUMAN), 774 aa.	0	
7043	cg43972840	929	AGACAAAGGTGC CCTGGAGGGCA GC[A/gap]GCTGT CCCTTCCGAACA GCTATGGC	A	gap	Ser	Ala (9214)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7044	cg43972840	953	CAGCTGTCCCTT CCGAACAGCTAT G[G/gap]CTGTGC TGAGGAAGCCCA GCCTCCA	G	gap	Ala	Leu (9215)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7045	cg43972840	1002	CAGTTCATCCTG GCCGCTGGTGT GG[C/gap]CCTAG CTGCTGGACTCT TGGCCTGG	C	gap	Ala	Ala (9216)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)

7046	cg43972840	753	AAGACCAAGAG AGGATCGTGA GG[A/gap]GGCCA ACAAGGCTTTTG AGTATAAC	A	gap	Glu	Gly (9217)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7047	cg43972840	913	TCTACGCTGCTG AACAAAGACAAAG GT[ gap]GCCCTG GAGGGCAGCAG CTGTCCCT	T	gap	Ala	Pro (9218)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7048	cg44010395	718	GGGAGCGGGTG TTGAGTGGGG CTT[C/gap]CCTC TGGGAGTCTCCA CGGGGGCAG	C	gap	Gly	Gly (9219)	FRAMES HIFT	oxygenase	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.[pcds:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.2E-151	22 (22q12)
7049	cg44010395	772	CTTGCACTTTGT TGCTGGCCCCGCT G[G/gap]CGAAGC CCTGGTGCCCCGT GAGGGGC	G	gap	Arg	Arg (9220)	FRAMES HIFT	oxygenase	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.[pcds:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.2E-151	22 (22q12)
7050	cg43916857	776	GCGCCCTCATCG AGTGGATCCGCA G[G/gap]AACAAAG TTTGCTTTCT GGAAATC	G	gap	Asn	Thr (9221)	FRAMES HIFT	peptidase	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.4E-96	17
7051	cg43254736	692	CATCTGGGGCTG TGCTGATGTCGT G[G/gap]CGAATG CCTTGACTGAG ATCCGGG	G	gap	Arg	Arg (9222)	FRAMES HIFT	peptidase	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.1E-67	

7052	cg42691989	846	CGAAGCCACATT CTCAATCAGCAC G[G/gap]CCCTGC CCCGGAACGTAT TGAAATC	G	gap	Ala	Ala (9223)	FRAMES HIFT	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101	14 (14q24.1)
7053	cg40084915	4336	CTCAGCAAAAAGC CAGGCCTTTGGG G[G/gap]CCCTCA TGGGCTCTGCG CATTGGT	G	gap	Ala	Ala (9224)	FRAMES HIFT	phosphatase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0	1
7054	cg42548845	2808	TGCGAGAACTGC TGAAAAATTCAG C[A/gap]AAAAAAT CATTGGATGAG AATATT	A	gap	Gln	Gln (9225)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0	
7055	cg42548845	2814	AACTGCTGAAAA ATTCAGCAAAAA A[A/gap]TCATTG GATGAGAAATATT CTAGCT	A	gap	Asn	Ile (9226)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0	
7056	cg43139469	885	TGGATAGCGACA ATCAATGACATA A[A/gap]ACTTCTC AATCAGACCCCTG GAACCTT	A	gap	Phe	Phe (9227)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7E-259	5 (5q31)
7057	cg43139469	886	GGATAGCGACAA TCAATGACATAA A[A/gap]CTTCTCA ATCAGACCCCTGG AACTTC	A	gap	Phe	Phe (9228)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7E-259	5 (5q31)

7058	cg43988365	2487	ACCATTTGCACT CGGGGAAGTAG TC[C/gap]TGGGG AAACTTCTCCTT CTCCAGCA	C	gap	Gln (9229)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa.[pcis:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
7059	cg43307302	949	TGGAAGAAGCTT TCTAAGGAAGAC T[gap]/TACCTCCT GCGTTTGATCAT TCACCA	gap	T	Leu (9230)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	8.7E-218 (18p11.3)	18
7060	cg42921141	90	CCTCCTCCTGGC CAGGGCAGCAA GC[C/gap]TTAGC CTTGGCTTCTTG TTTCIGCT	C	gap	Leu (9231)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P15309 PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) - HOMO SAPIENS (HUMAN), 386 aa.	6.8E-213	3 (3q21)
7061	cg43269274	1194	GAGACTGTTGAG TGGGTAGGCAC CG[G/gap]TGCCA GCACCGAGCA GGGAATGTG	G	gap	Arg (9232)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:Q16990 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
7062	cg43272594	663	GTCCAGTTCCTC CTGGTGGCCTTT G[C/gap]CCTCTA CGTGGGCTACAC CCGCGTG	C	gap	Ala (9233)	FRAMES HIFT	phosphatase	Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.4E-79	19

7063	cg43985274	612	AAGGCCAAGTTC TGTGAGGCCCC CG[G/gap]CAGCT GCGTGGCTGTG CACTGCGTG	G	gap	Gly	Ala (9234)	FRAMES HIFT	phosphat ase	Human Gene Similar to SPTREMBL- ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa.lpcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa.lpcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7064	cg43985274	650	TGTGCACTGCGT GGCGGGCCTGG GC[C/gap]GGGCT CCAGTCCTTGTG GCGCTGGC	C	gap	Arg	Gly (9235)	FRAMES HIFT	phosphat ase	Human Gene Similar to SPTREMBL- ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa.lpcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa.lpcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7065	cg43985274	675	CGGGCTCCAGT CCTTGCGCGCT GG[C/gap]CCTTA TTGAGAGCGGG ATGAAGTAC	C	gap	Ala	Ala (9236)	FRAMES HIFT	phosphat ase	Human Gene Similar to SPTREMBL- ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa.lpcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa.lpcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7066	cg43948077	1428	GGGGCAAGTTT GGGTATGGCATG G[G/gap]CAAGCC ACCGATGAGTGC TGTCCTCA	G	gap	Pro	Pro (9237)	FRAMES HIFT	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

7067	cg44005370	384	GACAGCCGGAG CGCCCGGCAAT GGC[G/gap]GCCT CGACGGCCTCG CACCGGCCCA	G	gap	Ala	Pro (9238)	FRAMES HIFT	phosphat aseinhib	Human Gene Homologous to SWISSPROT-ID:P41236 PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) - HOMO SAPIENS (HUMAN), 204 aa.	1.5E-105	
7068	cg43301213	490	CAAGGCTGGC ACCTCTGGGACA GC[A/gap]AAAA AACTGCAGAA GCATCCCT	A	gap	Lys	Lys (9239)	FRAMES HIFT	phosphat aseinhib	Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
7069	cg43301213	498	GGCACCTCTGG GACAGCAAAAA AA[A/gap]CTGCA GAATGCATCCCT AAAACTCA	A	gap	Asn	Thr (9240)	FRAMES HIFT	phosphat aseinhib	Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
7070	cg43988162	295	ATGAAGTAGCTC ACCAGCCGCTG CG[G/gap]CCTCT GCTGGTACTCGC TGAGCACA	G	gap	Pro	Arg (9241)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa.	1.8E-164	7
7071	cg43988162	449	AGGACTCCATCT CGATATTGCGGA C[G/gap]CCGGCT GCATAGGCTGCC TCCAGAT	G	gap	Gly	Gly (9242)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa.	1.8E-164	7
7072	cg43996195	1251	GAACCTGCCCTG CATCATCACACA G[G/gap]CCCTGC CATTCAAGGAACC CAAACAC	G	gap	Ala	Ala (9243)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	



7073	cg44022214	144	GTCCAGGGGGT CCGAAGCGCCG CAG[gap]AGCT GCTCCTGGTCTT CCAGGTCCT	G	gap	Leu	Leu (9244)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.lpcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
7074	cg44022214	281	ACTGCGTCCAGA GGCGCGAGAAG CG[gap/C]TCCTC CAGGGCATTTCAG ATGGGATA	gap	C	Arg	Ala (9245)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.lpcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
7075	cg43923788	547	CCTTTGTCTGAA TTCATTAGTGAT G[C/gap]TTTCAG CAAGTGGTGGC CTTGGTAA	C	gap	Ser	Thr (9246)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P56282 DNA POLYMERASE EPSILON SUBUNIT B (EC 2.7.7.7) (DNA POLYMERASE II SUBUNIT B) - HOMO SAPIENS (HUMAN), 527 aa.lpcis:TREMBLNEW- ID:G2832260 DNA POLYMERASE EPSILON SMALL SUBUNIT - HOMO SAPIENS (HUMAN), 527 aa.	1.2E-288	
7076	cg43968632	236	CTTTTTGAGTC AGGGGCCACG CC[gap/C]AGGCC TCCCAGGTCATC GTCCTCTG	gap	C	Leu	Leu (9247)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7

7077	cg43968632	295	CCCAGAAAGCT GATGGCTGGC AGG[C/gap]CAGG CTGCGCAGGTTC ACAAGGCAG	C	gap	Ala	Pro (9248)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7
7078	cg43968632	296	CCGAGAAGCTGA TGGGCTGGCAG GC[C/gap]AGGCT GCGCAGGTTCAC AAGGCAGG	C	gap	Leu	Leu (9249)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7
7079	cg43968623	1667	CCTGCCTTGTGA ACCTGCGCAGC CT[G/gap]GCCTG CCAGCCCATCAG CTTCTCGG	G	gap	Ala	Pro (9250)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
7080	cg43968623	529	GCGCAGCTTTAG CCGGCAGTATGC C[C/gap]ACATTTA TGCCACCCGCCT CATCCA	C	gap	His	Thr (9251)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
7081	cg43993893	579	GAACACCACAGT AATACTGATCTTT [gap]TJGGGTATC AACCTGATATCA ATTCTT	gap	T	Lys	Lys (9252)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)

7082	cg43993893	586	CACAGTAATACT GATCTTTGGTA TTC(gap)AACCTG ATATCAATTCCTC TGTGTG	C	gap	Leu	Leu (9253)	FRAMES HIFT	potassiu se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.jpds:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
7083	cg4333426	1585	CAGCCACCTGGA CCTGGAGCGCAT G[C/gap]AGGCTT CCCTCCCGCTG GACAACAT	C	gap	Gln	Arg (9254)	FRAMES HIFT	potassiu m_chann el	Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.jpds:SWISSPROT- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.4E-241	
7084	cg43008113	670	CGCATCACCGTG CAGGTCACCCGC A[G/gap]GCCGGT CCTCTACTTCCA CATCCGC	G	gap	Arg	Ser (9255)	FRAMES HIFT	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.jpds:TREMBLNEW-ID:G281120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.8E-180	1

7085	cg44131493	1304	GAAGAGTACTGC ATGGCCGTGTGT G[G/gap]CAGCGC CATGTCCCAAG TTTACTC	G	gap	Gly	Ala (9256)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa.   pcds:SWISSPROT-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa.	0	21
7086	cg43916732	1058	GCCCAAAGCAGT GCCGCCGGACA GG[C/gap]ACCTT GCAGAGCAACTT CTGTGCCA	C	gap	Thr	Pro (9257)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7
7087	cg43916732	773	GAGCCGTGAGC GACGACTCCCG GAG[G/gap]CTGG GGAGTTCTGCG GCGACGCAG	G	gap	Leu	Trp (9258)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7
7088	cg43916732	914	ACAAGACCCCTGC CGCGGGGCACT GC[C/gap]AAAGA AGGCAAGGGC CCGGCCCCA	C	gap	Lys	Lys (9259)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7
7089	cg42538037	1038	TCTGCCATGGAT GAAACTCAGAG A[gap/A]GAAAAG GAAGAGGGCCA TCAAACTC	gap	A	Arg	Lys (9260)	FRAMES HIFT	protease	Human Gene SWISSPROT-ID:P55085 PROTEINASE ACTIVATED RECEPTOR 2 PRECURSOR (PAR-2) - HOMO SAPIENS (HUMAN), 397 aa.	2.6E-207	5

7090	cg43921678	459	CTGGCTCCATG GATTGAGGCCTC TIG/gap]GCCGGA GCTGCCTGGTCC CAGAGTG	G	gap	Gln	Arg (9261)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	8.2E-185	15
7091	cg43921678	460	TGGCTCCATGG ATTGAGGCCTCT GIG/gap]CCGGAG CTGCCTGGTCCC AGAGTGG	G	gap	Gly	Gly (9262)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	8.2E-185	15
7092	cg43306871	642	ATCTGGGTGTAG ACAGCTGGATGC TIG/gap]GGCAGA GCCACAGGGGT AAACACCC	G	gap	Gln	Ser (9263)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
7093	cg43306871	644	CTGGGTGTAGAC AGCTGGATGCTG GIG/gap]CAGAGC CACAGGGGTAA CACCCCA	G	gap	Ala	Ala (9264)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
7094	cg43310246	2053	CTGGAGCTGGG ATTGTGGGCAG CGC/gap]CCCCG AGAAGGGGGTG CTGAAGGAG	C	gap	Ala	Ala (9265)	FRAMES HIFT	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa.	1.1E-141 (20p11.2)	20

7095	cg43930253	923	GAAAGACTGGCT AACTACACCGGA G[G/gap]CATCTA TGCCGAATACCA GGACACC	G	gap	Gly	Ala (9266)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7096	cg43930253	383	GACGGGCTGGC TCCGCTGGGGC GCA[G/gap]CACA TACCCCGGCCT CATGAGTAC	G	gap	Ser	Thr (9267)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7097	cg43930253	644	GGTAACGCTGG CTCCTGTGAAGG GG[G/gap]TAATG ACCTGTCCGTGT GGGACTAC	G	gap	Gly	Val (9268)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7098	cg44032168	1468	TTCTGGTGGGC CTGGTGAGCTG GG[G/gap]TGAGG GCTGTGGGCTC CTTCACAAC	G	gap	Gly	Val (9269)	FRAMES HIFT	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.4E-82 2 (2q13)	
7099	cg43921680	187	CTTACGCCAGAC TTCAGCCCTGCG G[G/gap]AGCTGC TGCCGCCAAAGA AAGCGGG	G	gap	Glu	Ser (9270)	FRAMES HIFT	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.6E-77	15
7100	cg43511784	115	CTCGTGGGGCAT CCTCCTGCTGGC A[G/gap]GCCGTG GCTGCCGTGTCC CTGTCTC	G	gap	Gly	Ala (9271)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7101	cg43511784	116	TCGTGGGGCATC CTCCTGCTGGCA G[G/gap]CCTGTG CTGCCCTGGTCCC TGCTCTC	G	gap	Gly	Ala (9272)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	

7102	cg43511784	126	TCCTCCTGCTGG CAGGCCTGTGCT G[C/gap]CTGGTC CCTGTCTCCCTG GCTGAGG	C	gap	Leu	Trp (9273)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1-PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7103	cg43511784	272	GCCTTCAGCCTA TACCGCCAGCTG G[C/gap]ACACCA GTCCAACAGCAC CAATATC	C	gap	Ala	Asp (9274)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1-PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7104	cg43268468	1212	CGCTCCCAGCG AGAGGCCGAG AGG[G/gap]CCGT GGCCACACTGA GAGGAGACAG	G	gap	Ala	Ala (9275)	FRAMES HIFT	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.8E-188 (17p13.3)	17
7105	cg43059041	1118	GACACGATTAAC AGGTGTCGCG AG[G/gap]CCTGA CCAGCAGCCAG GTGGACCTG	G	gap	Gly	Ala (9276)	FRAMES HIFT	protease nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1-PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.4E-83 (14q32.1)	14
7106	cg43969711	1380	CAATTCATCCCA ATGAGCTTCACA G[G/gap]CAAGGC CTCAGTGAGGAA CTCCTGT	G	gap	Pro	Leu (9277)	FRAMES HIFT	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.9E-208 2 (2p25)	
7107	cg43969711	1599	AATATCGACGCA AAAGAACCGGAA A[A/gap]GAAAT GCCTTCCACTGC AGCAAAAG	A	gap	Phe	Phe (9278)	FRAMES HIFT	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.9E-208 2 (2p25)	
7108	cg43941472	659	CCCGCACCAAGA CGGGAGTGGGG TA[C/gap]CCCCA GCTGAGTGCCGT CATTGAGT	C	gap	Pro	Pro (9279)	FRAMES HIFT	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184 X (Xq28)	

7109	cg43982619	411	GATGTGCTCTTC CTGGCTGTGAAG C[C/gap]ACACAT CATCCCTTCAT CCTGGAT	C	gap	Pro	His (9280)	FRAMES HIFT	reductas e	Human Gene SWISSPROT-ID:P32322 PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa.	4.2E-158	17
7110	cg43286949	965	CCTCATCCGCAC GGAGCCGGCTC GG[C/gap]CAACA CCAACCCACCACG ACGCCAAA	C	gap	Gly	Ala (9281)	FRAMES HIFT	reductas e	Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.lpcds:SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
7111	cg43948290	866	AATCATGGAGTG GTGTGGCTATGC C[C/gap]TGGCCA GCTGGTCTGTCC AAGGCGC	C	gap	Leu	Trp (9282)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa.	2.9E-141	5 (5p15)
7112	cg43921583	275	AGTGCCATTCTT TGGGGCATTCT G[C/gap]CACTGC AGCCCTCAGGC CTGCTGCA	C	gap	Ala	Ala (9283)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSNEW-ID:P30048 MITOCHONDRIAL THIOREDOXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa.lpcds:SWISSPROT-ID:P30048 MITOCHONDRIAL THIOREDOXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa.	1.2E-135	10



7113	cg43918176	911	CCACAAAGTCGCT CCGCCGTGGCC AG[gap]CCCAG GCCCCGAGGCTC CTCCGGTTA	gap	Gly	Gly (9284)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7114	cg43918176	917	GTGCTCCGCC GTGCCCAGGCC CAG[gap]CCCG AGGCTCCTCCG GTTATTACCG	gap	Gly	Gly (9285)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7115	cg43918176	928	GTGGCCAGGCC CAGGCCCGAGG CTC[C/gap]TCCG GTTATTACCGCC ACCAGGCC	gap	Gly	Glu (9286)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X

7116	cg43918176	943	CCCGAGGCTCCT CCGGTTATTACC G[C/gap]CACCAG GCCCTTCACGCT CCGACAC	gap	Ala	Arg (9287)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7117	cg43918176	450	ATCCCGAGCAAT GGGCAGTGTCTAT G[C/gap]CCACTA TTCCCCCCTTGG AAGCAGA	gap	Gly	Ala (9288)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7118	cg43927549	728	GCGCTCCTTTCC GTAACACACGGGA G[G/gap]CACGGC CGAGATGTACAC GAAGACA	gap	Gly	Ala (9289)	FRAMES HIFT	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIOLONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.6E-124 6 (6pter)	
7119	cg43332645	364	GACGTCCTGTT CTGGCTGTGAAG C[C/gap]ACATAT CATCCCCCTTCAT CCTGGAT	gap	Pro	His (9290)	FRAMES HIFT	reductase	Human Gene Similar to SWISSPROT- ID:P32322 PYRROLINE-5- CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa.	4.6E-65	1

7120	cg43936108	1407	AGAGGCCGGCG GGGGAGCAGA GTC[C/gap]TGGC GGCTTGGAACT CCGGCCTAG	C	gap	Arg (9291)	Arg (9291)	FRAMES HIFT	ribosomal prot	Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	2.5E-151	2
7121	cg43930758	566	TCGAATGACCAC TGCTGGATGTAC C[T/gap]TTTTCT GAGCTCTGGTT GCCTTT	T	gap	Lys	Arg (9292)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7122	cg43930758	722	GTTGTCAGCACA ATTGATTACAGC TTC[gap]CTACCG GAAGACCCAAAG GAAATCCG	C	gap	Gly	Glu (9293)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7123	cg43930758	723	TTGTCAGCACA TTGATTACAGCT C[C/gap]TACCGG AAGACCCAAAG AATCCGG	C	gap	Gly	Glu (9294)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7124	cg43255045	5827	AATCCCAAGAAG GGAAGGGCCAT GG[G/gap]CGGCT TCTGGAGCCCG GCACTCATC	G	gap	Arg	Gly (9295)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1

7125	cg43927378	6235	AAGGGAAGGC CCGGCCCCCG AGC[C/gap]GCTC AGCTCAAGCG CCCCTGCCC	C	gap	Arg	Ala (9296)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7126	cg43927378	6288	GAAGCCGCTTCT GCAGAGCTTCAC G[C/gap]TCCCGC ACAGCCCCGG CCCCCGCA	C	gap	Ser	Pro (9297)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7127	cg43927378	715	CGCGTGAACCA GTGCATCGTGTA TC[T/gap]CGGGT GAGAGCGGCTC CGGCAAGAC	T	gap	Ser	Arg (9298)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7128	cg43944016	2870	GGCTTGGCATTG CCCATGGGCTTC A[A/gap]GGGTCT CGGCAGGCTTG GCGTTGCC	A	gap	Leu	End (9299)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3
7129	cg43944016	642	CAAGGAAAGCTT GGGACACATCTT C[T/gap]TCAGATT CTAGTTTTCTG CATTGA	T	gap	Glu	Glu (9300)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3
7130	cg43944016	643	AAGGAAAGCTTG GGACACATCTTC TTT/gap]CAGATT TAGTTTTCTGC ATTGAG	T	gap	Glu	Glu (9301)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3

7131	cg43996806	3139	AACGCTCCCTCC CATATGGCACCG C[C/gap]ATGGAA AAAGCTCAGCTC AAGCCTC	C	gap	Met	Trp (9302)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa. pcds:SWISSPROT-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa.	0	12 (12q11)
7132	cg44033566	2968	GTGGACTCAGCC CTCCGAGTGCAC A[C/gap]ACTATG CGTAGATTGCGA GGAGACC	C	gap	Thr	Asn (9303)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
7133	cg44033566	2972	CTCAGCCCTCCG AGTGCACACACT A[gap]/CTGCGTA GATTGCGAGGA GACCAGCA	gap	C	Cys	Leu (9304)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
7134	cg42693827	2323	TGTGAACGTCAG AGTCTTGGACAC G[G/gap]CCAGGC CCAGTCCTCAAC CTGCGGC	G	gap	Ala	Pro (9305)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q10466 TTIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa.	0	2 (2q24.3)
7135	cg44001078	2033	AAGTTGAGCTTG GCCGAGAGCGA AC[C/gap]AAGGG CGTAGCCGTCAG GCACAAAC	C	gap	Gly	Val (9306)	FRAMES HIFT	struct	Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa.	0	

7136	cg43916919	297	TGCATGCGCGA GATGAAGCCCTC GG[C/gap]CAGCT GCAGGGCTGCC TGCCGCTCC	C	gap	Ala	Pro (9307)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.[pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)
7137	cg43304066	2303	TCAGTCCCAGTA ACCGGCCCTGG GG[gap]CJACCTC CAGCTCCAGCC GATAGGACA	gap	C	Val	Val (9308)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.2E-186	2
7138	cg43304066	2325	GGGGACCTCCA GCTCCAGCCGAT AG[G/gap]ACAGG TTCCTCAGGGTG CACACGCA	G	gap	Ser	Ser (9309)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.2E-186	2
7139	cg43918346	684	TGCAGTCAGAAG AGACTCGTGTGT G[G/gap]CACCGC CGGGATGGAAA GTGGCAGA	G	gap	His	Thr (9310)	FRAMES HIFT	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.4E-130	
7140	cg43980282	3863	CCTGGGCAGCA CCTCCGGGACT GAC[gap]CJTTCG GCAGTGGCTGG GGGACTGCTT	gap	C	Thr	Thr (9311)	FRAMES HIFT	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	3.9E-113	22

7141	cg43981852	662	CCGCAGTGAGAT G GAGGATCGGT CG[G/gap]CATCC CGCCCGCTCAC CCACTCCTC	gap	Ala (9312)	Ala	FRAMES HIFT	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.8E-113	
7142	cg43981852	812	GCGCTCATGCAG G TTTGTAGAACCG G[G/gap]CGATCT CGCACTTGCTGA CCTCCAG	gap	Ala (9313)	Ala	FRAMES HIFT	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.8E-113	
7143	cg42887734	249	CTGAAGAGCCTG C ATGCTGGCCAAG G[C/gap]CAAGGA ATGCTGGGAGCA GGAGCAC	gap	Ala (9314)	Ala	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7144	cg42887734	250	TGAAGAGCCTGA C TGCTGGCCAAG GC[C/gap]AAGGA ATGCTGGGAGCA GGAGCAC	gap	Arg (9315)	Lys	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7145	cg42887734	313	CTGAGAAAGGTGC G GCTACCTGGCAG A[G/gap]CGCATC CCCACGCTGCA GACCCGTG	gap	Ala (9316)	Arg	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7146	cg42887734	538	GTCGAGTCCGTG C TCTCGGCTGACG C[C/gap]ATGCTC CGGGCCCTGCT GGGCTCCA	gap	Cys (9317)	Met	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7147	cg42896604	695	ACTCCTCATTCT G TCACATTGAGGC G[G/gap]CCCCATG GCTGCGAAGGT GTCCCGAA	gap	Gly (9318)	Gly	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa.	8.6E-87	12 (12q23)

7148	cg42898003	516	CTCGTCCGTCAC GTGCTCCCCGG AG[G/gap]CCCTG AAAATCTCAGCC AGCTCCTC	G	gap	Ala (9319)	Ala	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.5E-80	20 (20q12)
7149	cg42898003	539	AGGCCCTGAAAA TCTCAGCCAGCT C[C/gap]TCCGGG TCGATGTAGCCG TCTGCAT	C	gap	Glu (9320)	Glu	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.5E-80	20 (20q12)
7150	cg43962741	1591	TATTGGCGTAAT GCTCTGAAAGAC G[C/gap]CCCCGG CCGTGGCTGCC CAGACGTA	C	gap	Ala (9321)	Gly	FRAMES HIFT	struct	Human Gene Similar to SWISSNEW- ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa.   pcls:SWISSPROT-ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa.	6.6E-73	3 (3q25.1)
7151	cg44014373	749	CAGTTCGTGGAT GTCACCTTGCT G[C/gap]TCTGCA CAGTGGCTGGA CTGGCTGC	C	gap	Thr (9322)	Ser	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
7152	cg43936426	729	TCAAGTAGTTTC CATCCAGCCGCA G[G/gap]TAGCGC AGGTGTGGCAC GTCTCCA	G	gap	Tyr (9323)	Tyr	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.6E-67	1 (1q32)
7153	cg43927885	422	GTGCAGATGCAC TCCAGGCGGGG GC[C/gap]TCCCA GTTTGAACAAG CGCAGCCA	C	gap	Pro (9324)	Ser	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.2E-55	17
7154	cg43961860	1112	AATGCTGCTTTT CCCCACATTTGG G[A/gap]AACCAC TTACTCCAACCC GAATGGC	A	gap	Ser (9325)	Phe	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	



7155	cg43961860	1137	AAACCAATTACT CCAACCCGAATG G[C/gap]TTTGCT GCAAGTTTCCTG AAAAACCT	C	gap	Ala	Pro (9326)	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	
7156	cg43248320	2488	TTTGATTACAGAA GTGGCGCCCCG GC[G/gap]GGCAG CAGCCCTCTTGC CCAAAGCC	G	gap	Arg	Arg (9327)	FRAMES HIFT	sulfotran sferase	Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N- DEACETYLASEN- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASEN- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa.	0	5 (5q32)
7157	cg44005661	2103	TTTCCACACCA GAAGTTGGGG TG[G/gap]CCGAG CCCACTCAATGA AAGGATGG	G	gap	Pro	His (9328)	FRAMES HIFT	sulfotran sferase	Human Gene SPTREMBL-ID:O00338 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa.lpcis:TREMBLNEW-ID:G2828824 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa.	5.4E-165	
7158	cg43972499	256	ATATCTAAGTGT GCTGCCCCCGTA G[G/gap]AGGCAC TGGAATTCCTTG CCCAGCA	G	gap	Pro	Leu (9329)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0	2
7159	cg43972499	588	GTCAATGTAGAGC ACATCAGTGTC G[G/gap]CAGCGC CTCCTCAATGCT CTCGAAT	G	gap	Pro	Leu (9330)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0	2

7160	cg40388639	1224	TGGCTCACTCCC CCATGCCAACGG C[C/gap]TGGCCC CCAGGCCCCCA GGCCAGGA	C	gap	Leu	Trp (9331)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7161	cg40388639	1232	TCCCCCATGCCA ACGGCCTGGCC CC[C/gap]AGGCC CCAGGCCAGG ACCCCGCGA	C	gap	Arg	Gly (9332)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7162	cg40388639	1245	CGGCCTGGCCC CCAGGCCCCCA GGC[C/gap]AGGA CCCCGCGAAGA AAGCAACCAG	C	gap	Gln	Arg (9333)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7163	cg43987111	2284	GCATGCTTTCTA TGTCCTCCACGG T[gap/T]CCACCA AGCTCAATAACA CACACTT	gap	T	Thr	Asn (9334)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
7164	cg43981333	403	GTCACATATCCAC CAGGCCCCCGCG CA[G/gap]CAGGG TAGATGGGAGAG AGGGAGAG	G	gap	Ala	Val (9335)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 919 aa.	0	19 (19q13.2)

7165	cg43948262	649	GCATTTTCCATT CCACTTTTGGAC A/gap/AAAGGGC CAGAAAGAAATTC TCATGA	gap	Phe	Leu (9336)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa.	0	21 (21q22.1 )
7166	cg43918681	911	CCACATCACACA GCTCTTCCAGTG G/G/gap/CACACC GCCCATCCATT GAATGGA	gap	Cys	Cys (9337)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0	3 (3p21.1)
7167	cg43918681	750	GATGTACCCTCC AACACAACCAA G/G/gap/CTTTGC CAAGTGTTCCAG AAATGAT	gap	Ala	Ala (9338)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0	3 (3p21.1)
7168	cg43976335	475	GCCCTCACACAG GGTATGGGTTGT C/C/gap/AGGACT GCCACTCCCGCT GCCACAC	gap	Leu	Leu (9339)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.3E-240	20 (20q11.2 )

7169	cg43959826	605	CATGGGGCTGG AGAGCCTTCCTG AT[G/gap]CCAGT GGCCAGGGCTT GTGGCGTGG	G	gap	Gly	Gly (9340)	FRAMES HIFT	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN-III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7E-140	10 (10q25.2)
7170	cg43959826	692	CGGCCAGCGCG CGAGCCGTAGT GGG[G/gap]CCGA TGGCTGCAAACT TAATTTGAT	G	gap	Gly	Gly (9341)	FRAMES HIFT	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN-III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7E-140	10 (10q25.2)
7171	cg43933068	500	CAAGGCTGGCTT GGTGGATGACTT TG[G/gap]AGAAGA AGTTTAATGCGC TGAAGGT	G	gap	Glu	Arg (9342)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
7172	cg43933068	502	AGGCTGGCTTG GTGGATGACTTT GA[G/gap]AAGAA GTTTAATGCGCT GAAGGTTT	G	gap	Lys	Arg (9343)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
7173	cg43963566	109	CAAGCCCACCCC TCACCTGGCCTT G[C/gap]CCTGGG CAGCCACAGCCT CCATGGC	C	gap	Gly	Ala (9344)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa.	9.3E-74	

7174	cg43963566	577	TTCTGCCTTGTT GAGGCCTGTGA GG[C/gap]CCCCG TAATGCCGCTCA TTGAGGCG	C	gap	Gly	Ala (9345)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa.	9.3E-74	
7175	cg44017251	1064	CTGTGGGTGAG GGCTGGGGCAG CGG[C/gap]TGCC GCATCCAGCAGT GCCCCGGCA	C	gap	Cys	Ala (9346)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7176	cg44017251	1118	AGACAGCTGAGT ACCAGTCATTGT G[C/gap]CCTCAC GGCCGGGGCTA CCTGGCGC	C	gap	Pro	Leu (9347)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7177	cg44017251	1120	ACAGCTGAGTAC CAGTCATTGTGC C[C/gap]TCACGG CCGGGGCTACC TGGCGCCC	C	gap	Pro	Leu (9348)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7178	cg44017251	1161	CCTGGCGGCCA GTGGAGACCTGA GC[C/gap]TCCGG AGAGACGTGGA CGAATGTCA	C	gap	Leu	Ser (9349)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	

7179	cg44017251	1521	CAGCCACCCCTCG GCTGGACCGTCA G[G/gap]CCACCT ACACAGAGTGCT GCTGCCT	G	gap	Ala	Pro (9350)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7180	cg44017251	887	CTGCTAGCCCCG TTCTGCCCCGCA G[G/gap]CCACCT CCGCCACCCCT GCCCCGCC	G	gap	Pro	His (9351)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7181	cg44017251	937	CGACCCAGCACA CCTAGGCAGGG CC[C/gap]TGTGG GGAGTGGGCGC CGGGAGTGC	C	gap	Pro	Leu (9352)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7182	cg43931248	1787	TGGAAGTGGATC CACGAGCCCAA GG[G/gap]CTACC ATGCCAACTTCT GCCTCGGG	G	gap	Gly	Ala (9353)	FRAMES HIFT	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
7183	cg43980446	10250	CTTCACGTTCCC AGCCTCCAAAT G[gap/G]CGTCCG CCCCATGGCTCG TGTAAGA	gap	G	Arg	Arg (9354)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1 )	15
7184	cg43980446	2708	AGGTGAAGCTTC CAGGAGTGTCT G[G/gap]CAAAATG CCCTTAGACCCG CACAGAT	G	gap	Cys	Cys (9355)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1 )	15

7185	cg43272560	829	ACAGGAGGTGC ATGTCCTGAATC TC[C/gap]GCACT GCAGGCCAGGG GCTGGCCAG	C	gap	Arg	Ala (9356)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
7186	cg43272560	837	TGCATGTCCTGA ATCTCCGCACTG C[A/gap]GGCCAG GGCTGGCCAG CTACAGAG	A	gap	Arg	Gly (9357)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
7187	cg43982633	1191	TGATTTTGTGGT TATGTGGCTGGA A[G/gap]CACCGA GACCTTCTTTT CATAATT	G	gap	Ala	Val (9358)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
7188	cg43918322	1060	GTCGTGACCAAG ACGCTACGGAG GT[gap/C]CCCAG GGGATCGCCG CGGTCGCCA	gap	C	Asp	Gly (9359)	FRAMES HIFT	thioester ase	Human Gene Similar to SPTREMBL- ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI GI: 1213545 - CAENORHABDITIS ELEGANS, 343 aa.	1.1E-53	20
7189	cg36988276	790	GCATTCATGGA ACCCAACTAGAT G[C/gap]AGTGAA TCTAAGCGATAA TAATAAT	C	gap	Ala	Glu (9360)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
7190	cg36988276	792	TTCAATGGAACC CAACTAGATGCA G[gap/C]TGAATC TAAGCGATAATA ATAATTT	gap	C	Val	Ala (9361)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)

7191	cg43300806	1000	CCAAAGGCCAGC CGCAGCTCTGAG AA[G/gap]TCGCT GGCGCTGCTCAA GACCGTAA	G	gap	Ser	Arg (9362)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P21453 PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 - HOMO SAPIENS (HUMAN), 381 aa.   pcis:TREMBLNEW- ID:G2668608 G PROTEIN-COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 381 aa (fragment).	9.4E-200	22 (22q13)
7192	cg43967090	1249	TTTCTTAAGCAC TTTTCAGAGCGA G[G/gap]CCGAGC CCCAGTCTAAGT CCCAGTC	G	gap	Ala	Pro (9363)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7193	cg43967090	923	CAGATTCGGAGG ATCATGGCTGCG G[C/gap]CAAACC CAAGCACGACTG GACGAGG	C	gap	Ala	Ala (9364)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7194	cg43967090	924	AGATTCGGAGG TCATGGCTGCGG C[C/gap]AAACCC AAGCACGACTGG ACGAGGT	C	gap	Lys	Asn (9365)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7195	cg42908704	924	CGCGGGAGGAG GTCAGCAGGACA AG[gap/A]GTGCG GGGCGCCGAAG GATAGCAAG	gap	A	Arg	Arg (9366)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P48663 B1 BRADYKININ RECEPTOR (BK-1 RECEPTOR) - HOMO SAPIENS (HUMAN), 353 aa.	7E-188	14 (14q32.1)
7196	cg43040271	1239	TACGTGAACAAG AGGACGCCCCCG GC[G/gap]CGCCG CTGCGCTCATCT CGCTCACT	G	gap	Arg	Pro (9367)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.   pcis:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	



7197	cg43040271	1243	TGAACAAGAGGA CGCCCCGGCGC GC[C/gap]GCTGC GCTCATCTCGCT CACTTGGC	C	gap	Ala	Leu (9368)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.   pcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
7198	cg43040271	1245	AACAAGAGGACG CCCCGGCGCGC CG[C/gap]TGCGC TCATCTCGCTCA CTTGCTT	C	gap	Ala	Val (9369)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.   pcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
7199	cg43962131	2093	GTGGCCACACTG CGCCTGGAAGG GC[C/gap]TGCGG AGGACGTTTCTG CAGGCGGA	C	gap	Arg	Ser (9370)	FRAMES HIFT	tnfirecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.2E-257	9
7200	cg42700065	108	TGAAGGAGCGCT TCCTACCGTTAG G[G/gap]AACTCT GGGACAGAGC GCCCCGGC	G	gap	Asn	Thr (9371)	FRAMES HIFT	tnfirecept or	Human Gene TREMBLNEW- ID:G2957264 TNF RELATED TRAIL RECEPTOR - HOMO SAPIENS (HUMAN), 299 aa.	2.3E-164	8
7201	cg43988937	768	TTCTGGCTCGTC CTTGCCCCCTTG G[G/gap]AGCCAA GAGACCCCTTCC CTTCTT	G	gap	Ser	Ser (9372)	FRAMES HIFT	traffic	Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa.	0 5 (5q32)	

7202	cg43934374	2836	AGGTTTCATCTA GAGGCAGAACAA G[C/gap]AGTACT AATGAAGATGAG GATTGA	C	gap	Ser	Val (9373)	FRAMES HIFT	transcript factor	Human Gene SWISSNEW-ID:Q99081 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.lpcis:SWISSPROT-ID:Q99081 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0	15 (15q21)
7203	cg43321351	2475	CAGGGCCTCCG GAGGGGCCCGC TGG[G/gap]CAGG CCTTCTGAATCT TGTGCTGAA	G	gap	Ala	Ala (9374)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1E-290	
7204	cg43321351	538	CAGTGCCCTCGC TGATGGCCGAG GC[C/gap]AGCGT CATGGCCACCTG CTCTGTCA	C	gap	Leu	Leu (9375)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1E-290	
7205	cg42896335	318	GCTCGGGGCC CCAGCAAGTCCC CC[G/gap]GTCGT CCCCGCAGGCC GCCTTCACC	G	gap	Arg	Arg (9376)	FRAMES HIFT	transcript factor	Human Gene TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	2.1E-285	12
7206	cg43947662	505	TGATATGATAGC TATCATTGGTTT C[gap/C]TGCTTT CATTGTGTCCAG AATAAAA	gap	C	Glu	Gly (9377)	FRAMES HIFT	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.7E-276	12
7207	cg43917801	840	ACGGAAGCGCT GCTGGCCGGCG AGA[gap/G]CTCG GACTCGGGCGC CGGCCTCGAG	gap	G	Asp	Glu (9378)	FRAMES HIFT	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.3E-249	6 (6p22.3)

7208	cg43920700	1283	TGCTTGCTGGAG TCAGACCAGGGA G[C/gap]CCCCGG GCCACAGCATCA GCCCTGC	C	gap	Pro	Pro (9379)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NFI-X) (NF-IX) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.1E-243	19 (19p13.3)
7209	cg21646034	870	TCCAATCTTCA GAAACTCCAGTA GT[gap]GGCCAC AGAAAGAGTAGT TACTGCA	T	gap	Val	Gly (9380)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9E-179	15
7210	cg43950592	97	CGCAGCAAACTT CGGGGGCGGC GG[C/gap]GGCAA CTCCACCGCG CGGCGGCGG	C	gap	Gly	Ala (9381)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:P48431 TRANSCRIPTION FACTOR SOX-2 - HOMO SAPIENS (HUMAN), 317 aa.	4.7E-173	3 (3q26.3)
7211	cg43929348	739	GATGAAGGCCA GGGATAAATTC AA[G/gap]AGTTG CTTCGGACACT TCCCTTTC	G	gap	Leu	Leu (9382)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
7212	cg43929348	746	CCAGGGATAAAT TTCAAGAGTTGC T[gap]CTTCGGA CACTCCCTTTC TGCTCTT	gap	C	Lys	Arg (9383)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
7213	cg43935763	742	CAGGCAGACACT TTCAGTTCTTTT T[gap]CTTGGCT TTCAGCACTGGA GGCAGA	T	gap	Lys	Lys (9384)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q13889 BASIC TRANSCRIPTION FACTOR 2, 35 KD SUBUNIT - HOMO SAPIENS (HUMAN), 303 aa.	1E-161	
7214	cg43982109	1793	GTCGACTCCAC AGCCGGTGCAC AG[C/gap]TCTGC TCCAGACCTCC CAGGGCAC	C	gap	Glu	Asp (9385)	FRAMES HIFT	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.6E-131	10 (7p)

7215	cg44028769	482	GGTGCTCACAA CCACCGTCCGCA G[G]gapJAGGCAA ACTTCAGGGACA GCACGCA	G	gap	Ser (9386)	FRAMES HIFT	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa.	4.6E-119	1
7216	cg43918209	1675	AGCGACAGCTG CAGACTCCGGTG CA[G]gapJCCGCA GGCCACCGCGC TGCAATGCGG	G	gap	Leu	FRAMES HIFT	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.7E-115	19
7217	cg43297584	707	TCCGCTGGCAAC AGTGCTCCCAAT A[gap/A]GCCCA TGCCATGCTGC ACATTGG	gap	A	Ser	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7218	cg43297584	785	TGTCATTGACAA CATTATGCGTCT G[G]gapJACGATG TCCTTGGCTACA TCAATCC	G	gap	Asp	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7219	cg43297584	793	CAACATTATGCG TCTGGACGATGT C[gap/T]CTTGGC TACATCAATCCT GAAATGC	gap	T	Leu	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7220	cg43917302	1568	ACCAGGCGGTG CACACTGGCAGC CG[C]gapJCCCCA CGCCTGCGCCG TCTGCGCCC	C	gap	Pro	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q81751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.   pcds:SWISSPROT- ID:Q81751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7

7221	cg43917302	1572	GGCGGTGCACA CTGGCAGCCGC CCC[C/gap]ACGC CTGGCCCGTCTG CGCCCGCAG	C	gap	His	Thr (9392)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7222	cg43917302	1590	CCGCCCCACG CCTGCGCGTCT GC[G/gap]CCCGC AGCTTCAGCTCC AAAACCAA	G	gap	Ala	Pro (9393)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7223	cg43917302	1652	ACCAGGCGATCC ACACAGGCTCCC G[C/gap]CCCTTC TCCTGCCCCGAG TGCGGAA	C	gap	Pro	Pro (9394)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7224	cg29214653	587	CCGGGACGGTT CTCTGCTAGCTC CC[T/gap]AACTG CTTCTGGCCAGG AGTCCAGT	T	gap	Leu	Gln (9395)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSPROT- ID:P50548 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - HOMO SAPIENS (HUMAN), 548 aa.	4.9E-68	1
7225	cg43917396	2228	CATGCGTTTGGG CATCTCAGGGTC G[G/gap]CCTTGC CCGCCACCATCC AGCGCGA	G	gap	Ala	Ala (9396)	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.9E-68	

7226	cg43944978	1414	AACAGGCCCGC AGATGCCCGCAG GTC[C/gap]TTCCG GCACCGTCTCCA GGGCCATCT	C	gap	Lys (9397)	FRAMES HIFT	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.4E-60	17
7227	cg43946772	3292	CATGAACCTGGTA CTTTTAGTTTTT [T/gap]CACATAA CTCTCTAAAGGC CTTTTC	T	gap	Lys (9398)	FRAMES HIFT	transfe se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1, O N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
7228	cg43935558	3108	ACAGTATGCACA AAACATGGGCCT G[C/gap]CCCAGA ACCGTATCATTT TTTCACC	C	gap	Pro (9399)	FRAMES HIFT	transfe se	Human Gene SWISSNEW-ID:P56558 UDP-N-ACETYLGLUCOSAMINE-- PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERAS E 110 KD SUBUNIT (EC 2.4.1.-) (O- GLCNAC TRANSFERASE P110 SUBUNIT) - RATTUS NORVEGICUS (RAT), 1036 aa.   pcls: TREMBLNEW- ID:G1931579 O-GLCNAC TRANSFERASE, P110 SUBUNIT - RATTUS NORVEGICUS (RAT), 1036 aa.	0	
7229	cg43916882	1905	ACCAAAAGAGGG CCCAAGCCCGG GC[C/gap]GCGGT GCTGGGCTCCAT CTTCCTCC	C	gap	Ala (9400)	FRAMES HIFT	transfe se	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.3E-245	1

7230	cg2537639	258	CACCTAGGAAGG ATGTCCTCGTGG TG[gap]ACCCCT TGGCTGGCTCCC ATTGTCT	gap	Thr	Pro (9401)	FRAMES HIFT	transferase	Human Gene SWISSPROT-ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA-N- ACETYL GALACTOSAMINYLTRANSFER ASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.5E-192	9 (9q34)
7231	cg43258046	1453	GCCACAGCCTGT GCACCTGCTGCC C[C]gap]TGCACG GGATACAGCATC TCAACAT	gap	Leu	Cys (9402)	FRAMES HIFT	transferase	Human Gene Homologous to TREMBLNEW-ID:G2673984 LEGITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment).	3.2E-146	16 (16q22.1)
7232	cg43949162	1194	CTTCCGTTGGGA TAGTGGAGCTTG G[G]gap]CCTTGC TGCCATGATAGC TTTTCAG	gap	Pro	Pro (9403)	FRAMES HIFT	transferase	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.3E-115	6
7233	cg43933127	1862	CTGGATCTGTGA TACTTGCTGTGT G[A]gap]CTGCCG TCTGGAGCTGTT CATTITG	gap	Val	Ala (9404)	FRAMES HIFT	transport	Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa.	0	4
7234	cg40351913	1680	TCCAGCAGATGA CCGGCAGCGG CC[C]gap]AGCCT GTACTGGCGGCT GTGCTGGA	gap	Ser	Ala (9405)	FRAMES HIFT	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
7235	cg43993573	252	GACGTCAGAAATG ATTCCTTGCAGA G[C]gap]CGCGCT GACCTTTGCCCG ATGTCTG	gap	Ala	Ala (9406)	FRAMES HIFT	transport	Human Gene SWISSPROT-ID:P52569 LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) - HOMO SAPIENS (HUMAN), 658 aa.	0	8 (8p22)

7236	cg44011204	1168	CAGGATGAAACG GCTGATGTGCTT G[G]gap]CCACGC CATTATTCTCCT CCACGCA	G	gap	Ala (9407)	Ala	IFAMES HIFT	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa	6.9E-197	
7237	cg44025532	678	CTGTGCACGCG GCTGGCCATCAT GG[gap]G]TGAAC GGTCGCCTGCG GTGCCTGGG	gap	G	Gly (9408)	Val	IFAMES HIFT	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.8E-174	
7238	cg43945806	307	AAACTCTGGTCT GGAAGAAATCAGT C[A]gap]CCTGAG CAAGGCTTCCGG AAGTAGA	A	gap	Gly (9409)	Gly	IFAMES HIFT	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
7239	cg43945806	432	AGATCTGAGGGC AGTCCGTTCCGG G[G]gap]TACCCA ATAGGCAATTGC TGTGTAG	G	gap	Pro (9410)	Pro	IFAMES HIFT	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
7240	cg43928832	1562	CGGTGGGGACA TGGCAACAGCC GCA[G]gap]CACC GGGTGCTGTAGA ACCGGTCAC	G	gap	Cys (9411)	Cys	IFAMES HIFT	transport	Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	2E-126	2
7241	cg43061328	262	CTGCAACAGGAA AACATTGTTCC C[C]gap]AGATGC TGGAGATGCAA GTAAGGC	C	gap	Trp (9412)	Trp	IFAMES HIFT	transport	Human Gene Homologous to TREMBLNEW-ID:E315451 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 552 aa.	5.6E-125	



7242	cg43331724	414	GTGCCCTTGGAC TTGCAGACCGTG A[G/gap]GACAGT ATTGGCTGTGT TGGGAAG	G	gap	Arg (9413)	Arg	FRAMES HIFT	transport	Human Gene Similar to SPTRMBL- ID:Q61185 KIDNEY-SPECIFIC TRANSPORT PROTEIN - MUS MUSCULUS (MOUSE), 545 aa.	1.2E-55	
7243	cg43990999	427	TTCCCTATCCCA GCTATGGTGTGT G[G/gap]CACTGC CTTCTTCATCAAT TTCATA	G	gap	Gly (9414)	Ala (9414)	FRAMES HIFT	transport	Human Gene Similar to SWISSPROT- ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa.	7.5E-55	10
7244	cg43986426	1241	TAAGCAGTGCAA GGTGTCTTGAGC C[C/gap]TATGGT GGCCATGCTGG GTGCAGTA	C	gap	Tyr (9415)	Met (9415)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7245	cg43986426	1251	AAGGTGTCTTGA GCCCTATGGTGG C[C/gap]ATGCTG GGTGCAGTAGCT GCCCAGG	C	gap	His (9416)	Met (9416)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7246	cg43986426	1261	GAGCCCTATGGT GGCCATGCTGG GT[G/gap]CAGTA GCTGCCCAGGA AGTGCTGAA	G	gap	Cys (9417)	Ser (9417)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7247	cg43986426	2004	TAGCACAGCCGA GCACACCCCTGCA G[T/gap]TGGGCC CGGCATGAGTTT GAAGAAC	T	gap	Trp (9418)	Gly (9418)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1

7248	cg43986426	2361	ACCTCCTCTACG TACTGGCAGCTG C[C/gap]AACCTG TATGCCCCAGATG CATGGGC	C	gap	Asn	Thr (9419)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7249	cg43986426	2761	AGCAGCTGTGG CAGGCCTGTTGG GC[C/gap]TGGAG CTGTATAAGGTG GTGAGTGG	C	gap	Leu	Trp (9420)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7250	cg43291895	702	TCATCCGGAAGC AGGTCCTGGGG AC[C/gap]AAGGT GGACGCGGAGC GTGACGGCG	C	gap	Lys	Arg (9421)	FRAMES HIFT	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.5E-129	
7251	cg44923887	2517	AGAGTATTCTTC AGCTAGGTCAGC C[C/gap]GAAGCG GGTGCTCAGGCT GGGGGTC	C	gap	Arg	Arg (9422)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4E-82	22
7252	cg44923887	2870	CTTCAAGCTCCT TCATCAGCCTCC TTG[gap]CTGGCC GCCATCTTGGAT TTGGTGC	G	gap	Ser	Arg (9423)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4E-82	22

7253	cg43939935	2099	GCAATGACCACA TGAAAATAACGG G[C/gap]GTTGCT CTCATCTGGTTC GGCTTTG	C	gap	Ala	Pro (9424)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa. pcls:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN). 152 aa.	7.7E-79	12
7254	cg43939935	2173	CAAACGCTGGGT TTCCCTTGATGAT C[C/gap]TGCGGG GCAGCCCGGCC ATCTTGTC	C	gap	Arg	Arg (9425)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa. pcls:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN). 152 aa.	7.7E-79	12
7255	cg43974851	1430	GTGGGGGAGTT GAGCAGGTGCC GCA[G/gap]GATG ATGGAGCGGTC CATGATGGTG	G	gap	Leu	Cys (9426)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). 961 aa.	1E-70	1
7256	cg43974851	1431	TGGGGGAGTTG AGCAGGTGCCG CAG[G/gap]ATGA TGGAGCGGTC ATGATGGTGC	G	gap	Ile	Ile (9427)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). 961 aa.	1E-70	1

7257	cg43921289	1307	CAGCTGGCAGC CAAGGAGGCCA AAG[C/gap]TTCG AGACCTGGAGG ACTCACTGGC	C	gap	Leu	Phe (9428)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7258	cg43921289	1794	GGAGATGATCCC TTGCTGACTTAC C[G/gap]GTTCCC ACCAAAGTTCAC CCTGAAG	G	gap	Arg	Arg (9429)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7259	cg43921289	1795	GAGATGATCCCT TGCTGACTTACC G[G/gap]TTCACA CCAAAGTTCACC CTGAAGG	G	gap	Phe	Ser (9430)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7260	cg43921289	1856	GGTGACGATCTG GGCTGCAGGAG CT[G/gap]GGGCC ACCCACAGCCCC CCTACCGA	G	gap	Gly	Gly (9431)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7261	cg43921289	2045	TGGAGATGACCT GCTCCATCACCA C[C/gap]ACGTGA GTGGTAGCCGC CGCTGAGG	C	gap	His	Thr (9432)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7262	cg43929067	2129	GTAGGACACTGC TGGAGCTGAGTG G[C/gap]TTCACA GCGCAATGACA GCAGCGT	C	gap	Lys	Asn (9433)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
7263	cg43929067	4145	GTCGCCCTTGGT ACATGTGGAATA G[gap/A]AAAAA AATAGCAGTCTT CTCCTTG	gap	A	Phe	Phe (9434)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

7264	cg43929067	4153	TGGTACATGTGG AATAGAAAAAA A[gap/A]TAGCAG TCTTCTCCTTGA TTAGGCA	gap	A	Phe (9435)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
7265	cg43969426	2748	GACCAAGTCTCA TTAGGCCAAGGC C[C/gap]ACAACT GCTCCTATCACC ATCTCCT	C	gap	Thr (9436)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0	1
7266	cg43924236	986	GCTTTCAAGCTG CATACGGTGGCC C[C/gap]AGTGGG GAGCGAGTCC ACGGACAA	C	gap	Leu (9437)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16632 TFIIIC2 SUBUNIT - HOMO SAPIENS (HUMAN), 911 aa.	0	2
7267	cg43925699	1687	CCGGGCCACTT CTGGCCACCG CA[G/gap]GCCCC TCGCCATGGCC GCTGGCCT	G	gap	Ala (9438)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
7268	cg44927137	1868	AGAGGAGTCTGA TGATGAAATAGC A[gap/A]GATAAG GATTCTGAAGAT AATTGGG	gap	A	Arg (9439)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
7269	cg44927137	1880	TGATGAAATAGC AGATAAGGATTC T[gap/T]GAAGAT AATTGGGATGAA GATGAGG	gap	T	End (9440)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
7270	cg43918935	306	AGGGACAGACG CACCGATCGCC GGA[G/gap]GGAC AGACACACGACC ACGGGGCGC	G	gap	Gly (9441)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3

7271	cg43918935	308	GGACAGACGCA CCGATCGCCGG AGG[G/gap]ACAG ACACACGACCAC GCGGCGCCA	G	gap	Thr	Gln (9442)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7272	cg43918935	337	GACACACGACCA CGCGCGCCAC CG[C/gap]CCACG CTCCACCCACC GCGGCCCA	C	gap	Ala	Ala (9443)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7273	cg43918935	415	TGGCACAAACTT TCCTCCCGGGAC G[G/gap]AACACG CTGCCTCAGGGA GCCCGCG	G	gap	Gly	Glu (9444)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7274	cg43918935	443	CACGCTGCCTCA GGAGCCCGCG AC[C/gap]GCGCC TTCTCCTCCGCC GGTCCCAT	C	gap	Ala	Arg (9445)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7275	cg43939697	414	AGATCCGCATGA AGGAGCTGGAG CG[G/gap]CACAG AAGGAGGTAGAA GAGAGACC	G	gap	Ala	His (9446)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3
7276	cg43940975	1352	CATCACCAGCTT CATCCGCTAGTGT G[G/gap]CCTCGC CCTCTGAAAACCT TGCCCTT	G	gap	Ala	Ala (9447)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3

7277	cg43940975	381	ACAGAGCAGTCC ACTAATGCTGCA T[C/gap]CACCAC GTGTAGTGATGC CAGGTTC	C	gap	Asp	Met (9448)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
7278	cg43940975	382	CAGAGCAGTCCA CTAATGCTGCAT C[C/gap]ACCACG TGTAGTGATGCC AGGTTCA	C	gap	Val	Val (9449)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
7279	cg44917921	3496	CCAGCCCCCAAA ACCAGCCTGGA GG[C/gap]ACTCA CTTCACAGGGTC CTGCCACA	C	gap	Ala	Asp (9450)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75162 KIAA0675 PROTEIN - HOMO SAPIENS (HUMAN), 1208 aa.	0	3
7280	cg43930961	1504	ATCTTTAACTCA TTTTTTTTTTTTT gap/AAAAGGAGG ACATTGTAAACA AGTG	T	gap	Lys	Lys (9451)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
7281	cg43935402	1165	AGCAACTCTTAC AGAGGGCAAAA Algap/A]GGGGC TCAAAAGAAAT TGAAAAA	gap	A	Lys	Lys (9452)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
7282	cg43935402	412	ATCGGCACCAAC CTGCGCCGGTTC C[G/gap]GGCCGT GTTTGGGGAGA GCGGCGGG	G	gap	Arg	Arg (9453)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4

7283	cg43935402	973	ACAGAAAGGATA AAGACCCCTTCG GG[ <i>gap</i> ]TCTCCT CATTAATTCTGA ACTGGAA	G	gap	Gly	Val (9454)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
7284	cg43924112	1967	TGTTGTTCAGA AACTAAAACTG GIC[ <i>gap</i> ]TTTGCT GCACCTTGATCA GCTGTAG	C	gap	Lys	Asn (9455)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
7285	cg43925091	228	ACCCCAAGTCTA GGGCTACCGGA AG[G[ <i>gap</i> ]TAGAG AAGCTCTGGGTG GCAGTGCA	G	gap	Thr	Thr (9456)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHEICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0	6
7286	cg43929503	1035	GCTGCGGGGTC GCAGGCTTTGCC GG[ <i>gap</i> /C]CTTCC ACGCAGGAGCA GACCCCACG	gap	C	Ala	Gly (9457)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
7287	cg43929503	1349	CCAGTGCCGAG GCTCCATTCCGC AC[C[ <i>gap</i> ]TCCGG CAGGTCGGACAT CGTGTCTC	C	gap	Glu	Glu (9458)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
7288	cg44036171	2202	TGGAGTGATTCA GCACACAGGCG CA[G[ <i>gap</i> ]CAGCT GAAGAAATTTAAT GATGATAC	G	gap	Ala	Gln (9459)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75485 MULTIPLE MEMBRANE SPANNING RECEPTOR TRC8 - HOMO SAPIENS (HUMAN), 664 aa.	0	8



7289	cg43958488	1801	GCAGGTGCTCAT CCTTGGCGGAG GC[C/gap]AACAA ATGTTACATTTT GCTTCCC	C	gap	Leu	Leu (9460)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
7290	cg43923753	3157	TATGGTCCAGAC CTTCTTGGGGT G[G/gap]CTGCTG CCTTCTCCTCCT CTGAGTC	G	gap	Ala	Ala (9461)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7291	cg43923753	3690	CTTTCGCTCTGG GACCTTGGCAGA C[gap/C]TTGAGC CAGAAAGCTATAG ATGTCTA	gap	C	Asn	Lys (9462)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7292	cg43923753	3733	GATGTCTAAGAG GGAAGAGGCATT G[G/gap]CATCCT GCTGTGTAGCTC CTGTGCGC	G	gap	Ala	Ala (9463)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7293	cg43925880	769	CACCTTGCAGCT CAGGAGCCGGG CC[C/gap]TTCCG GCTCATAACCGT GGACATGT	C	gap	Lys	Lys (9464)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13435 SPICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa.	0	11
7294	cg43966967	1484	GGGCGTCGGGC GGGACAGTGGA AGA[G/gap]AGAG GGACTTTGCCTA CGTAGCTCG	G	gap	Glu	Arg (9465)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11

7295	cg43966967	1486	GCCTCGGGCGG GACAGTGGAAGA GA[G/gap]AGGA CTTGCCTACGT AGCTCGTG	G	gap	Arg	Gly (9466)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11
7296	cg43966967	1490	CGGGCGGGACA GTGGAAGAGAG AGG[G/gap]ACTT TGCCTACGTAGC TCGTGATAA	G	gap	Asp	Thr (9467)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11
7297	cg43334182	5146	AGGGGCTGTCT GCTGTATTCCT GCT/gap]GCACA CTTGAGGGTGGA TATACCCC	T	gap	Gln	Arg (9468)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa.	0	12
7298	cg43916884	993	AAACCTTCCTG GCCAAAGTCTAG G[C/gap]CCGTGG GCACCAGTCGCA CATTCTCT	C	gap	Gly	Ala (9469)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
7299	cg43916884	287	GAGACACAGTG GGAGGCTGAGG CCC[C/gap]TTGG GGGTATCATTCT GTTCTGGA	C	gap	Lys	Lys (9470)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
7300	cg43932638	324	TGCCTCCATCCA CCGGGGCTATG GC[C/gap]GCAGA AGAGGTATTGCA GACGGTGG	C	gap	Ala	Gln (9471)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa.	0	12

7301	cg44918447	608	AAATCTTTTCAGG CTATGGCTTTTTT [gap]/TGTCTCTT GGCCTTATATCC TGGACG	gap	T	Gln (9472)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
7302	cg43961443	539	CGCCGCCTCGT CCAGGTCCAGCA GC[C/gap]TCCGG TTGACCTCCAGT GTCATGCA	C	gap	Arg (9473)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa.	0	13
7303	cg43968223	774	GCTGCCTGGCA GTGCAGATGAGC CG[G/gap]CTGAT GCCCTCAATGCA CTGGCTCT	G	gap	Ser (9474)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
7304	cg44022133	3698	GAGAGGGACAG GGAGAGAGAGA GAG[gap]/AAGG GAGCGGGACAG GGGGACCGA	gap	A	Arg (9475)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0	14
7305	cg43055918	485	AGGGGGCCTGG GCTTTGGAGGG GCC[C/gap]GCAG AGCGCTGGCATA GGACATGGC	C	gap	Arg (9476)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
7306	cg43949150	887	AGATGAACCTCT TAAGCACATTCT T[G/gap]GGAAGG ATGTAGGTGTAG CCAGTCT	G	gap	Pro (9477)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
7307	cg44023800	352	GCCTGGACGCT CAGCCACTCACT CT[gap]/CTCCGC CATTGCTGAGGC TGCACCCC	gap	C	Glu (9478)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa.	0	17

7308	cg44001797	3902	GCTATCTTCCTG AAAGGCTGCATA G[C/gap]CTTCAG TCCTCTTTTCCTT TTTCCT	C	gap	Gly	Ala (9479)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP78 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
7309	cg43917942	1322	GGGGTTCACG CATGCCCCCGG GGG[G/gap]CCGA GGCCGAGGAAG AGGCCAAGGC	G	gap	Gly	Ala (9480)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7310	cg43917942	1491	TAGAGATCTCCC GGCAGCTGCCA CC[C/gap]AACGG GGACCCCAACTT CAAGTTGT	C	gap	Asn	Thr (9481)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7311	cg43917942	1498	CTCCCGGCAGCT GCCACCCAACG GG[G/gap]ACCCG AACTTCAAGTTG TTCATCAT	G	gap	Asp	Thr (9482)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7312	cg43917942	1616	TGCCCAGTTGGA CCAGGCCACG TG[G/gap]CCCAG GCCCTGCTGGC CCAATGGGG	G	gap	Gly	Ala (9483)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7313	cg43917942	1641	GCCCAGGCCCT GCTGGCCCAATG GG[G/gap]CCCTT CAATCCTGGGCC CTTCAACC	G	gap	Pro	Pro (9484)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19

7314	cg43917942	1892	CCCGGGCCCCCGC ACCGGGCCCCCTG CGG[C/gap]CCCCA CCGGCTCAGGG TGAGCCCCCT	C	gap	Ala	Ala (9485)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7315	cg43917942	1912	TGCGGGCCCCAC CGGCTCAGGGT GAG[C/gap]CCCC TCAGCCCCCACC CACCGGCCA	C	gap	Pro	Pro (9486)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7316	cg43917942	1916	GCCCCACCGGC TCAGGGTGAGC CCC[C/gap]TCAG CCCCACCCACC GGCCAGTCG	C	gap	Pro	Leu (9487)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7317	cg43917942	2077	GAAGCAAGCGC AAGTGGCCACC GGA[G/gap]GGG GTCCAGGAGCTC CCCCAGGCTC	G	gap	Gly	Gly (9488)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7318	cg43975166	820	GGAGTGGGTATT CTGGTAGCCTGC T[G/gap]GGCTTG GCGCCACCTGG TGGTAGCT	G	gap	Pro	Gln (9489)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa.	0	19
7319	cg43991657	1308	CTCTGGGCTGG GGCTGAGGATTG CG[G/gap]CCCTG GGGCAGCTTCTC CTTCCCA	G	gap	Pro	Arg (9490)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19

7320	cg43991657	335	CCTGAGGCGTG CCCAGGCTCTG GCC[C/gap]GGGC AGCAGGGGTGA GGCAGGGGCT	C	gap	Arg	Arg (9491)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7321	cg43991657	443	CTGCTCCCAGG GGCCCTGGCGG GCG[G/gap]CCTG GGCCGGCCCTG CCCAGACAGC	G	gap	Ala	Ala (9492)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7322	cg43991657	568	GAGTAGGGGTTT CTGGGCGCTTGA G[C/gap]CGCCTT TGCAGTCGGAG GGCAGGCC	C	gap	Arg	Arg (9493)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7323	cg43919691	1070	GGCAAGCTCATC GCTCTGTTTCTG G[G/gap]CTTCGC TCTTGGCGGCAT CGAGCTG	G	gap	Ala	Ala (9494)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7324	cg43919691	701	CTTCAGAAAGCTC CTGCAGTCTCGT G[G/gap]CGGCGC GCCCCAGGTCA CTTGTTAA	G	gap	Ala	Ala (9495)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7325	cg43919691	709	GCTCCTGCAGTC TCGTGGCGGCG CG[C/gap]CCCAG GTCAC TTGTTAA CTTCTTCT	C	gap	Gly	Gly (9496)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7326	cg43921598	1826	ACAAGGACTGG GAGCGGCACCA CCG[C/gap]CTCT GTGGTCAGAACCC TGCATGGCC	C	gap	Leu	Ser (9497)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa.	0	20

7327	cg43918155	1307	GTAAAGAAAGAG AAGGACAGAGA GG[G/gap]CAGCA GCCTGAAGAAGA AGTGTTTG	G	gap	Gly	Ala (9498)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14241 ELONGIN A - HOMO SAPIENS (HUMAN), 772 aa.	0	1 (1p36.1)
7328	cg43968854	893	CAATGTC TTGAC AATAGCAAAAA A[gap]/AJTAAATCT CCCTTTTGAAG CTTTAT	gap	A	Asn	Lys (9499)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
7329	cg43973740	1103	GATTGCTATTTT TAGAGCTTTTIT T[gap]AGGCACTC CATTACCCTCTT GCCTC	T	gap	Leu	Leu (9500)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0	16 (12q12)
7330	cg44928323	4878	TTGAGGAATTTA TGACTAGGCATC A[gap]/TJGGTACA TGAAAAAGAAAGA ATTCAAG	gap	T	Gln	His (9501)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
7331	cg43948022	921	CTGTCACGGTGT CCCCAGGCCCC CA[G/gap]GTGGC TGCGCACTGCAT CCTCAGTG	G	gap	Leu	Trp (9502)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7332	cg43948022	922	GTCACGGTGTCC CCAGCCCCCA GG[gap]/GJTGCT GCGCACTGCATC CTCAGTGT	gap	G	His	His (9503)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7333	cg43948022	703	GGGGCACAAAC AAGGTCAACTGA GG[G/gap]CCCCG GGCTGGCCAATA GCGGCCAA	G	gap	Gly	Gly (9504)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)

7334	cg43948022	713	CAAGGTCAACTG AGGGCCCCGGG CT[G/gap]GCCAA TAGCGGCCAAG GTAAAGCC	G	gap	Pro	Gln (9505)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7335	cg43955232	838	AGCAGCAGCAG CAGCAGCAGCA GCA[G/gap]CACC TCAGCAGGGCTC CGGGGCTCA	G	gap	His	Thr (9506)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa.	0	6 (6p23)
7336	cg42907760	1681	CATCCCCCTCAC CTTCGGCGGAC CG[G/gap]CGGCG CCAGCTTCGTGC CCCTGGAG	G	gap	Arg	Gly (9507)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
7337	cg43311566	1080	CCAACCTCCACC CTGACGGCCGC GC[C/gap]ATGGC CACCAAGTTTGC ACACTTGA	C	gap	Met	Trp (9508)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
7338	cg43311566	856	CAAGGATGTACT GCGCACTGACC GG[G/gap]CCCAC CCCTACTATGCG GGGCCTGA	G	gap	Ala	Pro (9509)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
7339	cg43921793	1032	CTGCGAGGGAG CTGATAGGCTGG AA[G/gap]CTATTT TTGAAGTTTCTT TTTGT	G	gap	Ser	Ser (9510)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
7340	cg43921793	1318	CTGGGGGTCTATA GTAGTAGCCGGA G[G/gap]TCTCAT CGTACTGGTAGG TAGAGAC	G	gap	Thr	Thr (9511)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X



7341	cg43921793	364	GCCCCCGTGCAC CCAGGCCGGAG CCC[C/gap]GCAC CCGTGTTGGGC CTCGATAGG	C	gap	Arg (9512)	Arg (9512)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
7342	cg42682094	289	CATAGTAGAGAA GGGGGCCCCCT GG[gap/G]CCTGC TCCAAGCCAGCC TTGCAGCA	gap	G	Gly (9513)	Gly (9513)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
7343	cg42682094	3085	GACAGACTGCTG TGAGGACAGGG CT[gap/C]GGCGC AGAGCGAGCAG TCACAGGTG	gap	C	Ser (9514)	Glu (9514)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
7344	cg43032555	1098	AGAGCTTGGCC GTCTCTTGGGG TC[C/gap]TTCCG GTCATTACCTC AAAGTGCC	C	gap	Lys (9515)	Lys (9515)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0	
7345	cg43032555	189	CCACTGGCACCC TTCTGCCCCAGGG G[C/gap]TGACCC TCGGGCCCCATC CCCAGCA	C	gap	Gln (9516)	His (9516)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0	
7346	cg43303383	1243	ACAGACTTTATT GTGGGGGGGT CC[C/gap]ACCTG GGACCCACCTC TTAAATAA	C	gap	Trp (9517)	Trp (9517)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	

7347	cg43303383	1383	GGGCTGGAGGG GTGGAGGCAGG GCC[C/gap]TTGT CACCTGCATGCC CACATCCAC	C	gap	Lys (9518)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7348	cg43303383	1455	AGATGCTCTGGG AGGGGCTAGGG AG[gap/C]CCCCA GGCTAGGGGCA AGATGGCAG	gap	C	Gly (9519)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7349	cg43303383	664	CTGAGGCCGAG TCGCTCGCCGCT GC[G/gap]GGCTC TGATTGAGATGG TGGTGGCA	G	gap	Pro (9520)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7350	cg43927175	134	AGCATCTTCTGG AATAGGCGCATG G[C/gap]CTCATC CACCTTCCTGAG CTCTGCT	C	gap	Pro (9521)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21819 G7A - HOMO SAPIENS (HUMAN), 1264 aa.	0	
7351	cg43932090	1755	CCATGTCGGACA CTTCCTCCTCCT C[C/gap]TCTAAAT CTTCTAGGTCCT CCTTGT	C	gap	Glu (9522)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
7352	cg43932090	1757	ATGTCGGACACT TCCTCCTCCTCC T[C/gap]TAAATCT TCTAGGTCCTCC TTGTCA	C	gap	Arg (9523)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
7353	cg43940146	354	ATGCCGAGATAC TTCAGGGCATCA G[C/gap]CTGGCT GTATCTGTAATC AAAAAC	C	gap	Leu (9524)	IFRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa.	0	

7354	cg43940465	5447	CTGAGGGCTCG GTCATGCTGGTT TC[C/gap]TTCGG CTGCTCAGAGAC TTCACATA	C	gap	Lys	Lys (9525)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0	
7355	cg43966585	1546	CAAGCACCTGCG CCTGTCCCTGAA C[G/gap]GCCACG GCCAGTGTACAG TACAGCA	G	gap	Gly	Ala (9526)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7356	cg43966585	1547	AAGCACCTGCGC CTGTCCCTGAAC G[G/gap]CCACGG CCAGTGTACAGT ACAGCAT	G	gap	Gly	Ala (9527)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7357	cg43966585	1643	CACCCCATCCCA CTGGAGTCAGG GG[G/gap]CTCGG CCGACATCACCC TTCCGAGC	G	gap	Gly	Ala (9528)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7358	cg43966585	1701	GGCCCCAGGAC CCCCACCAGA GCC[G/gap]GGCC CCACGCCCCCT GCCGGCCCCG	G	gap	Gly	Ala (9529)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7359	cg43966585	1703	GCCCAGGACCC CCCACCAGAGC CGG[G/gap]CCCC ACGCCCCCTGC CGCGCCCCGG	G	gap	Gly	Ala (9530)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7360	cg43966585	867	TC TTCGTGCCGC CCAAAGCCTCCA G[G/gap]CCCAAG GTCAGCATCCCA CTGTCAG	G	gap	Pro	Pro (9531)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	

7361	cg44003855	393	CTCCTGGGTGGT GCCACCGGAGC CC[C/gap]GGCCC AGCTTCTTCTCC ATCTCCCC	C	gap	Arg	Gly (9532)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49841 ALPHA-MANNOSIDASE IIX (EC 3.2.1.114) (MANNOSYL- OLIGOSACCHARIDE 1,3-1,6-ALPHA- MANNOSIDASE) (MAN IIX) - Homo sapiens (Human), 1139 aa.	0	
7362	cg44011100	566	CAAGCTCCTGGG GAGGGGGCCCT GC[C/gap]GCAGG GCTTCCCTTC CCTCTCCA	C	gap	Ala	Ala (9533)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15450 P160 - HOMO SAPIENS (HUMAN), 1251 aa.	0	
7363	cg44016445	1446	GGGCTCCCTGC CCCGCTGCAGC CCC[gap]CTGCT TGGGAGGCACT GGACTTAGGC	gap	C	Arg	Arg (9534)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa.	0	
7364	cg44024279	1732	ATGCCAACAGGA GGCCATGCTTCA G[C/gap]AGCTTG GTGGTGGATGAA ACATATG	C	gap	Ser	Ala (9535)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
7365	cg44024279	1850	CTGCAACGATG AAGCAAGAGTTT C[gap]CTCATTAA CCTTGTAAGCA AAAGCC	gap	C	Leu	Pro (9536)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
7366	cg44024279	1941	TTCTCAGGCCTG TTGGAGAAATGC T[G/gap]CCAAGG CCAGGAACAGG AAGTCTGC	G	gap	Cys	Ser (9537)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	

7367	cg44932543	319	TGTTGATCTGTC CCTCCTGGATTT C[C/gap]TGCCGG GTCTCGGCAGG CAGATGGT	C	gap	Gln (9538)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75341 BRCA1-ASSOCIATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 600 aa.	0	
7368	cg43957199	1189	CCGAGGAAATAT CAGGCTGATGG CT[G/gap]GGGCA GGCCCGGAGCT GGTAGTGTG	G	gap	Pro (9539)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1	1.0e-313
7369	cg44002959	4273	GGCTGCCTCGTC CGGGGTCTCAG GG[G/gap]CCAGT GGCGGGGGGCT TTCAGGGGT	G	gap	Ala (9540)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment).	5	1.4e-316
7370	cg43937128	832	CTGGTTTTTCATT CCATTCTTGCT[ G/gap]CCTTTTGG CTGTATCTCTCC ACGAG	G	gap	Glu (9541)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	X	4.0e-317
7371	cg43937128	504	TGTGAAAGGTGC TTATCTCGTTGT C[C/gap]TTCGGA GTTGCCCTGCTGA CTGTTTC	C	gap	Lys (9542)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	X	4.0e-317
7372	cg44015618	837	AGGACAGAGGA CAGTGAGGGAC AGG[G/gap]CTGG GGCCAAAAGAAAT TAACAGATC	G	gap	Ser (9543)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	11	8.7e-312

7373	cg43923376	1635	CCCCAGGCTCTG GCCCAGAGCAG GG[G/gap]CTGTT GCCGAAAGGCT GTGGAGCAA	G	gap	Ala	Leu (9544)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
7374	cg43981656	1518	AGTCTCTTTCCG TTTGCCACCAGA A[A/gap]GGCTT TGTCCTCGCTC TTGGGAT	A	gap	Leu	Leu (9545)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
7375	cg44128920	1189	ATGAGAAGACAC CTCAGATGGG GA[C/gap]CCCCG CAGCTTGAGCC CCAGATCG	C	gap	Pro	Pro (9546)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7376	cg44128920	1418	GGACACCAGG AGAGCTCTGAAG AG[C/gap]CTCCC TCAGAAAGAGAGC CAGGACAC	C	gap	Pro	Leu (9547)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7377	cg44128920	1520	CATAGGTCAC TG TGTGGCCATCTA C[C/gap]ACTTTG AAGGTCACGC GAGGGCAC	C	gap	His	Thr (9548)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7378	cg43949262	1272	GGGTCCCGCTG AAGCTGCCCAG GGC[C/gap]TGCG GGTCGCTCTGAA TGCCCTTCA	C	gap	Gln	Gln (9549)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	

7379	cg43949262	770	CAGCAGGCACC AGGCTGGGGCA CCA[G/gap]CTGG GGCCTGGGTAC GCCCAGAAAG	G	gap	Leu	Trp (9550)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
7380	cg43931799	2153	GCTGGGGGTCT GAACCCGAACCA GG[G/gap]CCTGA ACAGGCTGATGC TGGCTGTG	G	gap	Gly	Ala (9551)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment).	7.6E-289	22
7381	cg44010409	1496	GACGAGCAGAA CTGCCAGTGGT GGG[G/gap]CGGT AGCCAGGCAAG CTGAGCAGGG	G	gap	Arg	Arg (9552)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
7382	cg43930921	1135	CAATCTCAAAGA AGGAGATGGTG CC[C/gap]TTGCG GTAATCTCATT GCCTGGAG	C	gap	Lys	Lys (9553)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
7383	cg43930921	877	CATAGCTGAAC CGATCAGCAGCT TT[G/gap]CCGTAG CCCCGGCGCTG GTAGGGAG	G	gap	Gly	Gly (9554)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92893 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
7384	cg44001088	352	GGTCACACACA GTGACCGGACG AA[G/gap]TTGTT CCAATTGGTTTT CCAATGCA	G	gap	Leu	Phe (9555)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
7385	cg44001088	469	TTTGCCTCTTTAT TTTTGCGGATAG[ C/gap]AGTTTGAA TGGCCTTCTTCT GTTTG	C	gap	Ala	Leu (9556)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X

7386	cg44022026	1703	CCCAGGGGTGTG CTGGAGCACCAC AC[C/gap]TACGG CGCCCTGCTCTT CCCACTGC	C	gap	Tyr	Thr (9557)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa.	1.2E-278	8
7387	cg43252100	1461	TCTAACATTTTC ATCAGCCTATGG [C/gap]AAGTGGT TTTGTGGATTTT CTAAA	C	gap	Ala	Glu (9558)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BA83037 KIAA1085 PROTEIN - HOMO SAPIENS (HUMAN), 584 aa (fragment).	4.9E-278	
7388	cg43922691	188	GGCCGGACTGG AAAGCCGGAGC GGG[G/gap]CCAG GCGGGCCTCCC CAAAAGCCTG	G	gap	Pro	Gln (9559)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7389	cg43922691	324	GCTCCGGCAGC GGAACCGCCTG AGG[C/gap]TGGA GGAGGACAAAC CGGCCGTGGA	C	gap	Leu	Trp (9560)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7390	cg43922691	353	AGGAGGACAAAC CGGCCGTGGAG CG[G/gap]TGCTT GGAGGAGCTGG TCTTCGGCG	G	gap	Cys	Ala (9561)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7391	cg43988211	1246	ACCCAAATCGAA TCCATAGGCTGC G[C/gap]CAGGGG CCTGTTATCATG TAATAGG	C	gap	Trp	Cys (9562)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
7392	cg43958878	131	GGTGATGGGTTG GTCTCAGCGGA T[G/gap]CCTTGG TGGATGAGGCTG CTTTTGG	G	gap	Gly	Gly (9563)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9



7393	cg43958878	1461	TTTGCCAGGAGT TCGGCCCCGAG TC[C/gap]TGCCG GCGCTGTGGA TCGGTTGGC	C	gap	Arg (9564)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7394	cg43958878	1510	CGGCCCGCATG GGTGAGGGGC CGG[gap/G]CCTG CGGCTTCCCTGG CTTCGCTG	gap	G	Pro (9565)	Pro	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7395	cg43958878	1530	GCCGGCCTGCG GCTTCCCTGGCT TT[gap/G]CGCTG CCAGCGCGCAG GGGTGCAT	gap	G	Ala (9566)	Glu	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7396	cg43958878	247	AGGGTCTCATCT GCTGCTGCGGAT G[C/gap]CACTGT GGCCCATCTG GGCTCATG	C	gap	His (9567)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7397	cg43153237	244	CCAGCCCTGGT GCTGGGGGTGG CCC[C/gap]TTGTG CCTGGGTTGTGG CCAGCCCCCT	C	gap	Cys (9568)	Leu	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60540 HYALURONIDASE - HOMO SAPIENS (HUMAN), 463 aa.	1E-267	
7398	cg43967058	536	CCTTCCAGGAGG GCGCGCGGGC CC[gap/C]GTTGG AACAAATTTCGT GGATAGGC	gap	C	Pro (9569)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X

7399	cg43967058	541	CAGAGGGCGC GGCGGCCCGT TGG[gap]/G/AACA AATTTCGTGGAT AGGCTGCCT	gap	G	Asn	Glu (9570)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X
7400	cg43967058	570	AATTTCGTGGAT AGGCTGCCTCAG G[gap]/C/JAGTTAG AAATCGTGTGCA AGCGCTT	gap	C	Gly	Gly (9571)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X
7401	cg43980328	1085	CTGAAAGAGATC ATCATCACTGCT G[G/gap]/CCTCGC CTAGAGCAGGAA ACATGGG	G	gap	Ala	Ala (9572)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
7402	cg43922182	1381	GCTGCTGCTCGA CAGCCCCACGTC G[C/gap]/GCACGC CGCCGCCGCC TCCTGCTC	C	gap	Arg	Ala (9573)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7403	cg43922182	1570	CCTGCTGGCGC CGGGGGCCCCG TGC[G/gap]/CGGC CTGCTCGTCGGC CTCGTGCGC	G	gap	Ala	Arg (9574)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7404	cg43922182	1958	TCTGAGTCTCCC AGCCTCGACCCCT G[G/gap]/CCGCCG CCTGCCAATCTT CAGCCCGC	G	gap	Gly	Ala (9575)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7405	cg43922648	2335	GCCAGTAATGGA CACCTGTCTGTT G[G/gap]/CTTTGC CCAGAGCAGCA GTCCCCTTT	G	gap	Ala	Ala (9576)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15054 HYPOTHETICAL PROTEIN KIAA0039 - Homo sapiens (Human), 491 aa (fragment).	3.3E-260	11

7406	cg43980777	1028	CAATCTGGGGTC GTGAGCAAGTG GC[gap]/CJTCTT GGCCCTCCTTTT CATCATTT	gap	C	Ala	Gly (9577)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
7407	cg43929959	195	AAGAAACATGT CAGGACACAAAT G[gap]/CJTATCC CTGGGACTTACA GGATCGA	gap	C	Cys	Cys (9578)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78506 DIABETES MELLITUS TYPE I AUTOANTIGEN (ISLET CELL AUTOANTIGEN P69) - HOMO SAPIENS (HUMAN), 483 aa.	2.1E-258	7
7408	cg43254094	1287	CCGGCTCCAGCT AGGAATGCTGCA G[C/gap]AAGCAC AGTGTGGCCTTG ATCTTCG	C	gap	Gln	Lys (9579)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7409	cg43254094	267	CCGGCTCTGCTG CTGCTGCTGCTG C[gap]/TGGCTCC CGCCACAGCCGC AGCTTCCC	gap	T	Arg	Leu (9580)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7410	cg43254094	803	CCAACAACTGA CAGTCCGGGTGT C[C/gap]TGGGAG ACACCCGAAGGA AGAGACA	C	gap	Trp	Gly (9581)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7411	cg43986498	1366	GCTACATCTACC ACAGTGACATCG TG[gap]CAGTCC CTGCCACCGGAT CTGCCGC	G	gap	Gln	Ser (9582)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7412	cg43986498	1519	AGATCGAGCGCA AATTCGACAAAT G[G/gap]CAGGAG CCGCCGCCTGT GAAGCAGG	G	gap	Gln	Arg (9583)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19

7413	cg43986498	1950	CGGCAGAGAAG AAGGTGGCTGA GGC[C/gap]AACC AGAAATATTTCT CCAGCATGG	C	gap	Asn	Thr (9584)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7414	cg43986498	961	GCACGGTCAAG GAGCTGGGCAA CAG[C/gap]CTGG ACAAAGTCAAGA ACAATGAGA	C	gap	Leu	Trp (9585)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7415	cg43978430	1070	TACGACGCCACA TCTCTGCCCGCA G[G/gap]TGCAGA CCCACAGCAAGT GATCAAT	G	gap	Gly	Val (9586)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75879 CYTOCHROME OXIDASE ASSEMBLY FACTOR - HOMO SAPIENS (HUMAN), 557 aa.	2.8E-255	4
7416	cg44034555	470	GCGGAGTCTCAT GGGCAAGGGCT GGG[C/gap]CAAG GGGCTCCTTCCC GAAGTCCAC	C	gap	Gly	Ala (9587)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1
7417	cg44034555	471	CGGAGTCTCATG GGCAAGGGCTG GGC[C/gap]AAGG GGCTCCTTCCCG AAGTCCACC	C	gap	Gly	Ala (9588)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1
7418	cg39711096	893	CCGGGAGGCCCC ACAGTTACTGCC TC[C/gap]AGCTG CAGCAGTGACAT CGCTGACC	C	gap	Ser	Ala (9589)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1E-251	

7419	cg43254830	1275	CATTCCAAAGCT CTGACCCAGAAC A[G/gap]ATGCGA CAGAGTTTGCTG ACTGCAA	G	gap	Met	Cys (9590)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA7821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
7420	cg43254830	1323	CAATCCGTTCCG GAGAGGCTGCT GC[C/gap]AAATT GAAAAGGGTTAC CATTCCAT	C	gap	Lys	Asn (9591)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA7821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
7421	cg44910581	2889	CAAACTCTGAAG TGAACCTCATGAT C[gap]/AJGTAGA ATACCAGATCCT TATACTC	gap	A	Cys	Met (9592)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	
7422	cg43945969	303	GGAGGCCCTGC GCGCGCTCAGC GCG[C/gap]TCTT CAAAGAGCAGC GGAACCGAGA	C	gap	Leu	Ser (9593)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43383 HYPOTHETICAL 53.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	4.1E-246	22
7423	cg43980318	142	CAACGGCGATTG CGGCCGCCCA GG[G/gap]CGCG GCCCGGAGGAA ACCGGGTGAC	G	gap	Ala	Arg (9594)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7424	cg43980318	150	ATTGCGGCCGC CCCAGGCGCG GCC[C/gap]GGAG GAAACCGGGTG ACGGTGGTGC	C	gap	Gly	Glu (9595)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7425	cg43980318	231	GGAAGGTGGTG GACCTGCTGCG GCA[G/gap]GACG CCGACATCGTGT GCCGCTGCC	G	gap	Asp	Thr (9596)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)

7426	cg43980318	232	GAAGGTGGTGG ACCTGCTGGCG CAG[G/gap]ACGC CGACATCGTGTG CCGCTGCCA	G	gap	Asp	Thr (9597)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7427	cg43980318	237	TGGTGGACCTGC TGGCGCAGGAC GC[C/gap]GACAT CGTGTGCCGCT GCCAGGGAG	C	gap	Asp	Thr (9598)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7428	cg43980318	87	GCGTCACTGGA GCCATGGCGTTC GC[C/gap]GAGAC CTACCCGGCGG CATCCTCCC	C	gap	Glu	Arg (9599)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7429	cg43994815	358	GTCAGTGTCCAC CCCTGGCTGGG AG[G/gap]CAGAG CCGGACCTTCCT CGTGGACC	G	gap	Gln	Arg (9600)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa.	3E-236	10
7430	cg43994815	729	AGCCTGTCCAC GACAGGAGCTTC A[G/gap]CTACAC AGGGACAGCC AGGCGCAG	G	gap	Ser	Thr (9601)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa.	3E-236	10
7431	cg43932322	327	TGGTCCAGCCGT GGAAGGGCGG CA[gap]GICCGAT GCCTCGCCCATC GCGGTAC	gap	G	Cys	Leu (9602)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa.	6.5E-236	2
7432	cg43330158	1330	GAAGTCGCACAA GACCCGCAACCA G[gap]/C/JACAGGA CGAGGGGATCC TGCCCTCG	gap	C	Arg	Ser (9603)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	

7433	cg43330158	1332	AAGTCGCACAAG ACCCGCAACCAG A[C/gap]AGGACG AGGGGATCCTG CCCTCGGG	C	gap	Gln	Arg (9604)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
7434	cg43330158	1333	AGTCGCACAAGA CCCGCAACCAGA C[A/gap]GGACGA GGGGATCCTGC CCTCGGGC	A	gap	Gln	Arg (9605)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
7435	cg43930174	1376	CAGTGCTGCGG GGCCGCATGGT GCG[G/gap]TACC TGATGCGCTCGC GTGAGATCA	G	gap	Tyr	Thr (9608)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
7436	cg43948360	2451	CTCCATGTTGAG GGCCAGTCCTC G[C/gap]TCTGCA GGGAGCCATCT GTGGCTTT	C	gap	Ser	Thr (9607)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
7437	cg43952917	1353	TGGGCATTGACA GCAACCTGGGTT C[C/gap]TAACGG TTTGGTTAACAC CAGCACG	C	gap	Gly	Glu (9608)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q99611 SELENIDE:WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa.	1.5E-232	
7438	cg43940463	852	GTGCTCTTGGTA GTACTCCAGGAA G[G/gap]CGCGGC CCACACTCTGCG CCACCGG	G	gap	Ala	Ala (9609)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.1E-232	

7439	cg43947107	781	CCATGCGCACCC GCTGCCTCAGCT C[C/gap]TGCCGG CTCACCTCCTCC TTTGCCA	gap	Gln (9610)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa.	2.8E-231	3
7440	cg43948144	1163	TAAAAAGGCCAA GTTTCACCACTC T[G/gap]ATTGCC TTTCAACCTGGC TACTTCA	gap	Asp (9611)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
7441	cg43986279	2340	CTACCCGCTTCC GCGGCCCGAC TG[G/gap]CTGTG CCGCGTGGTGA AGCACCTGC	gap	Leu (9612)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa.	7.5E-231	12 (12q14)
7442	cg43986279	2588	GTCACCAAGGCC C GCGACTGCTG GG[C/gap]CACCT TCATCCAGCCCT GGGGTTCT	gap	Ala (9613)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa.	7.5E-231	12 (12q14)
7443	cg43916785	3222	GATCTGGATGCC CTTCTGCCAGAA G[G/gap]CGCTGC CTGATTTCCTCA AGCTCCT	gap	Arg (9614)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
7444	cg43933074	1068	CAGCTCCACCCT C GAAGTCGCTGCT G[C/gap]GCCCCC ACTTCTCAACA CGCCTGA	gap	Ala (9615)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19



7445	cg43933074	115	GTGCAGTTCTAC AAGGTGTGCGTG A[G/gap]CGTGGT GAGCGAGAAGT GCCGTATC	G	gap	Ser	Thr (9616)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19
7446	cg43933074	967	TCCACCCGGATC CTGGCCCATGAAG G[C/gap]CTCGCT CTGCAAGCTGTC GCCCTGC	C	gap	Ala	Ala (9617)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19
7447	cg43978295	756	TGCCAGGGATGA ATAGCCACTGGG G[C/gap]CCTGGC CATAGCTGGACT GTCTCTT	C	gap	Gly	Gly (9618)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
7448	cg43978295	758	CCAGGGATGAAT AGCCACTGGG CC[C/gap]TGGCC ATAGCTGGACTG TCTCTTC	C	gap	Gly	Gly (9619)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
7449	cg43918561	603	AGAGGACGTGC GCAGCCCCGCG GGG[G/gap]CCCA AGTCCCCCTGGT TCCCAAGAA	G	gap	Pro	Pro (9620)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224 (11p15.5)	11
7450	cg43994204	674	CGCACGTCAAGA CTGTCTGCGACG C[A/gap]GCAGAG AAGGGAGTGAG GACCCCTCA	A	gap	Ala	Gln (9621)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
7451	cg44032871	637	TGTGGTGGGGT CTCCTCGGAGCT GG[G/gap]CCCCTT GGCGGGGCAGC TGCAGAAAT	G	gap	Pro	Pro (9622)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5

7452	cg43960557	741	CAGGCTCTAGAA AGTCATCTGCTG C[C/gap]CCCCAG GTCCTCCAGGGA ATCCTCC	C	gap	Gly	Ala (9623)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
7453	cg43062833	1042	CTGGCCCCCAGAA AGGGGCTTTTGG C[C/gap]ACCAGC TTCAGAAAAACA TGGCAGC	C	gap	Pro	His (9624)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q83088 BETAINE--HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa.	2.1E-219	5
7454	cg43934903	894	CTGGAGCAAAAC CTCCCTGAAGTC C[C/gap]TGAGGG GCAATGTTCCAG GCAAGGT	C	gap	Gln	Gln (9625)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
7455	cg43251548	233	AGCTTCCTATGG ATCTGCGGGACC G[C/gap]TTCACG GAAATGCGCGA GATGGACC	C	gap	Phe	Ser (9626)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.7E-217	
7456	cg43251548	274	GAGATGGACCTG CAGGTGCAGAAT G[C/gap]AATGGA TCAACTAGAACA AAGAGTC	C	gap	Ala	Glu (9627)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.7E-217	
7457	cg43990581	262	CAGATCCTCAGC CACCGCTTCAAA G[C/gap]CTGTGC CCAGCAGGTC CAGTGAGC	C	gap	Ala	Ala (9628)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.6E-214	17
7458	cg43980581	263	AGATCCTCAGCC ACCGCTTCAAAG C[C/gap]TG TGCC CCAGCAGGTCCA GTGAGCT	C	gap	Cys	Val (9629)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.6E-214	17

7459	cg43062448	1362	GAATCCATAAAA TGGTGAAGTCCC A[gap]TGGAGCT CCACAAATGTAG CCAAATT	gap	T	Leu	His (9630)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
7460	cg43969195	156	TGGAGGAGCTG CTCGCAAAAGGCA GA[G/gap]CAGGA CGAGGCAGAGA AGTTGCAAC	G	gap	Gln	Arg (9631)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
7461	cg43332618	619	GTCACAGGGCA CCTCGAAGCTGA AA[G/gap]CTTCG TTGTAATAGGGG TTCAGAGT	G	gap	Ala	Val (9632)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O00445 SYNAPTOTAGMIN V - Homo sapiens (Human), 386 aa.	5.8E-208	19
7462	cg43932174	464	CACACTTCTTAT TCCTGGGCTTTA[ G/gap]CTCTTCGG CTGCATTACGCA GGAAA	G	gap	Leu	End (9633)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
7463	cg43995867	1174	GAAGAACTTGTA GAACATTACAAA A[A/gap]GGCACC AATTTTACAAGT GAACAA	A	gap	Lys	Arg (9634)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
7464	cg43920365	922	TGCTTTGTGAAT GGTGCTGGGCT CG[C/gap]CATGG CTACTTGTGATA TCATTTTC	C	gap	Ala	Ala (9635)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
7465	cg43968205	508	AGGGCCACGGA GACACACTGTAC GT[G/gap]GGGAC CACCCGCAATTC CATCCTGC	G	gap	Gly	Gly (9636)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment).	6.9E-206	

7466	cg43999733	1292	GGCCCGGCGCT GACACGGCCAG CTC[G/gap]GGCT CGCCCCGAAC TCCTCCCGGA	G	gap	Pro	Pro (9637)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7467	cg43999733	1310	CCAGCTCGGC TCGGCCCCGAA CTC[C/gap]TCCC GGAAGGCTCGC CGGGCCTCGG	C	gap	Glu	Glu (9638)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7468	cg43999733	1327	CCGAACCTCTCC CGGAAGGCTCG CC[G/gap]GGCCT CGGCCAGCAGC TCCGCGACC	G	gap	Arg	Gly (9639)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7469	cg43999733	464	AGCGGTGGCTCT CCACCATGAGGC G[G/gap]CCAAAG GCTCTGTAGTCG CCACGTC	G	gap	Gly	Gly (9640)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7470	cg43999733	614	GCTCTCCAGTT GTACCTCCCCGA G[G/gap]CTTTCC TTGCCACGCGCC CGGGCCA	G	gap	Ser	Ser (9641)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7471	cg43999733	659	GGCCACCTTCTT CACATTGGCGCC G[C/gap]CGCACA GGTACTCGCTG GAGGCCA	C	gap	Arg	Arg (9642)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)

7472	cg43999733	660	GGCCACTTCTTC ACATTGGCGCCG C[C/gap]GCACAG GGTACTCGCTGG AGGCCAG	C	gap	Arg (9643)	Arg (9643)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7473	cg43302693	632	GCAGCTGGCTTC GGCAGGCCGTC AG[G/gap]ACCCA GGAGGTGGCG CAGGGGTCA	G	gap	Pro	Leu (9644)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7474	cg43302693	671	GCGCAGGGGTC ATCCAGGATTG AG[G/gap]CCCTG GCCCCACCTGA GTGACAATG	G	gap	Pro	Leu (9645)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7475	cg43302693	678	GGTCATCCAGGA TTTGAGGCCCTG G[C/gap]CCCACC TGAGTGACAATG ATGTATT	C	gap	Gly	Gly (9646)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7476	cg43302693	681	CATCCAGGATT GAGGCCCTGGC CC[C/gap]ACCTG AGTGACAATGAT GTATTGA	C	gap	Val	Val (9647)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7477	cg43950996	2126	GTAGCTGATCCA GTCCAGAACCTG C[G/gap]TCTTCG ACCAGAACTGGG GCTGTTTC	G	gap	Thr	Ser (9648)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1

7478	cg43942842	2011	CATGAGGCCGAA CATGTTCCGCA G[G/gap]CCTTGC TCACCGCAGCCA TCTTGGC	G	gap	Ala (9649)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE,WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
7479	cg43942842	2730	GAATGACACAAG TATCCATTCCAA T[G/gap]CCAAGC CTTGGCATAACG GCTCCCA	G	gap	Gly (9650)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE,WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
7480	cg43959472	990	TGAGGTAGATGA TGACCACATTGT C[C/gap]TCCGGC CCTGATGGCTGC ACCTCGT	C	gap	Glu (9651)	Glu	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
7481	cg43918848	2198	ACGGCCTGTTGG TGACCTCAGCTC C[G/gap]GGCAGG GAATCCGTTGCA GTGCCG	G	gap	Pro (9652)	Pro	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
7482	cg43918848	2200	GGCCTGTTGGTG ACCTCAGCTCCG G[G/gap]CAGGGA ATCCGTTGCAGT GCCGGTC	G	gap	Pro (9653)	Pro	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
7483	cg44128902	825	CCTAGGAAAGG GAATACTCTCTA TG[gap]ATATATG GAGAAAGACATGA CACCCAC	gap	A	Asp (9654)	Val	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201 (1p36.2)	1
7484	cg43940298	804	GTCACCTGAATGA TAGGTGATTATG G[G/gap]CCCCGG GCACCTCCGCTT CTTATGA	G	gap	Pro (9655)	Pro	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15906 YL-1 PROTEIN - Homo sapiens (Human), 364 aa.	3.7E-197	1

7485	cg44015472	1167	ACTTGGATGTTG TCGGGCGGCGT TG[gap]CACAG GGCCAGCGCTC ACCGCCAGG	G	gap	Pro	Gln (9656)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (IT-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7486	cg44015472	618	CCTTCCTCTTCT TGGGGTAGCACA G[C/gap]CCTCCG GACTCTCGGGAT TAAGATG	C	gap	Ala	Leu (9657)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (IT-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7487	cg44015472	716	GGTGAAGATGGA GTCCTCAGGGAT G[C/gap]CCACAC CCTGGGCAACCA CTCTGAA	C	gap	Gly	Ala (9658)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (IT-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)

7488	cg44015472	771	TGCAGGAGAGT TCCCTCAGCTGC G[G/gap]CGCCCG CCCGTAGAGCTT GGCAGTA	G	gap	Pro	Arg (9659)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7489	cg43287442	765	CTGGGCAGAGT TTTGTCACAAA A[gap]/JTTCATTA TGCTGCAAGGC GTAAAT	gap	A	Phe	Phe (9660)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD09188 PLACENTA-SPECIFIC ATP-BINDING CASSETTE TRANSPORTER - HOMO SAPIENS (HUMAN), 655 aa.	3.1E-193	4
7490	cg43970111	1377	CCTGGCTGAGTC AGCTGGGGCTG AC[C/gap]TCCGG AGTCAGCCATCT TGAGGAAC	C	gap	Gly	Val (9661)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43131 SYLD709613 PROTEIN HOMO SAPIENS (HUMAN), 357 aa.	6.5E-193	14
7491	cg43935935	284	TTAGTCTTACG GCGTCAATAACA A[A/gap]TGCTTC AACATCATCAGC TCCAATC	A	gap	Phe	Leu (9662)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	1.7E-192	X
7492	cg43973314	638	ATGATCTGACTA ACTTCACTGATA TTT/gap]CCCCCT GGTGGAGTAGA GGAGAAAG	T	gap	Pro	Pro (9663)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
7493	cg43964795	1267	TGTTTCTTTTC AGCTCTTCAAAC[ C/gap]TCCGGGA AAGATCATCAAA GTCAAT	C	gap	Arg	Ser (9664)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16



7494	cg439968431	235	TCGTCGTCGCTG CCCTCGCCGCC CG[C/gap]GCCGC CCATCCGCTCCT CTCTGCTC	C	gap	Ala	Arg (9665)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7495	cg439968431	438	CACGCCTTGAC ATCTTCTTCATG G[gap/G]CCTTGG GAGCCAGGAACT GAGAAGA	gap	G	Ala	Ala (9666)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7496	cg439968431	500	CCACTTGGGTAA GGAGCCTTTGG GG[gap/G]TCCAC CTGGGCCAGGT AGGTGATGA	gap	G	Asp	Asp (9667)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7497	cg43920610	924	CAGGCCACCTGT TTCTTCCAAACA G[C/gap]TTTCAG CAACATGAACCT TCCCAT	C	gap	Ser	Thr (9668)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21
7498	cg43996402	1046	GGAAGAGGAGG AGGAGGAGGAA GAT[G/gap]AGGA AGAAGAGGACTT ATGTTTTT	G	gap	Ser	Tyr (9669)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7499	cg43996402	1220	TCAACTTCTGGA TCTTCTTCACCC T[gap/G]CAGTTG CAACATACTCCT GTGATGG	gap	G	Glu	Ala (9670)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7500	cg43996402	1249	TGCAACATATCTC CTGTGATGGATC A[gap/G]TTTGGC GTCAAGTTTCTC CCCAGTA	gap	G	Lys	Asn (9671)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2

7501	cg43996402	1300	ATTCGTTTCAG TGCAAAACCCACT Ggap/GjTTTCTC ATCTCCGCTATT AGCTCCG	gap	G	Lys	Asn (9672)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7502	cg43996402	1376	TCAGTGGGAACC GAACTTGCATTG Agap/CjTTCCAG AAAGACCAACA AAGGACA	gap	C	Ile	Ser (9673)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7503	cg43996402	1427	TTCTCGATCTGT GTTGACATGACC C[C]gap/ATTTGT GACATTTAATGC ACCTCAC	C	gap	Trp	Trp (9674)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7504	cg43996402	599	CTTCTGCTTTGC TCTTCACCAGGA Tlgap/GjTTTCGCT GTGCCCGTTTC TTGTCTC	gap	G	Asn	Thr (9675)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7505	cg43996402	962	TTTTCTTTCTTT TCTTCCTTTGTA gap/GjTTTTTTTT CTTTATTGTTACT CTC	gap	G	Ile	Thr (9676)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7506	cg44002198	1629	GAAGGGCCTCG GACTTCAGCGTG AG[G]gap]CCCCGA GGCGCCAGGG GCTGCTGCA	G	gap	Gly	Gly (9677)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
7507	cg44002198	1665	CCAGGGGCTGC TGCAGCAGGAAC AG[G]gap]CGAGG CCCGGAAACCA GCAGCGAGA	G	gap	Arg	Arg (9678)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7

7508	cg44002198	716	CTGGAGGACTCC TTGGAGCCTGCA G[gap/C]CCCCCTG GTGTCCCAAGGC CCCAGAA	gap	C	Leu	Ala (9679)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
7509	cg43249389	991	GATTGGGGCCG CCGACTACCCAGC CC[A/gap]CTGAG CAGGACATCCTC CGAACCAG	A gap	gap	Thr (9680)	Leu (9680)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.4E-188	15
7510	cg43947129	1222	TTTTTCTAAAGC ATCATCTCCTTT G[gap]GCATTGC CAATGCGGAATG GAATAT	G gap	gap	Ala	Ala (9681)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
7511	cg43947129	2137	GACCAGGCCCA AAGTTGACCACC TG[C/gap]CTGGG GGCGTCCATGGT GCGGCGGC	C gap	gap	Arg	Ser (9682)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
7512	cg43922383	660	CGATGCCATTGT GGCTAAGGTACA G[C/gap]TCCCGC AGGTTACCAGG TTCTGCA	C gap	gap	Glu	Asp (9683)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
7513	cg43047610	604	ACACTATCGAGG AGGGCACGATG CC[C/gap]AAGGA GATGCGGACAT CATCCAGC	C gap	gap	Lys	Arg (9684)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB37839 TRANSDUCIN ALPHA- SUBUNIT - HOMO SAPIENS (HUMAN), 350 aa.	7.3E-185 3 (3p21)	

7514	cg43950796	1309	GCGTGGGTCTC CCTACCCCACT TG[G/gap]CCATC GGCTCTCCTATC GCGGCGCC	G	gap	Ala (9685)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
7515	cg43950796	783	GCTCCTCAGTTT TCAGTGCTGGCT G[C/gap]CCCACT GGTCTACTGAC TCTCCAT	C	gap	Gly (9686)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
7516	cg44007066	1553	GCCTCTTGGGT TGGGCTCGGCC TG[C/gap]CTGCG GAAGTAGTCTGG CCCCTTGT	C	gap	Ser (9687)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB50224 HYPOTHETICAL 41.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 373 aa (fragment).	1.7E-183	
7517	cg44128927	599	GACCCAGCCAG AGGCCCTCCCGC GGA[G/gap]CCGG GACTGCAGAGTC GACCTGGGC	G	gap	Thr (9688)	Ser	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5
7518	cg43986952	1388	CAAACTGGCACT TGGCCCCGTAG CG[G/gap]CAGCG CCCACTCTCTGA GAAGGTCC	G	gap	Cys (9689)	Cys	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181	19 (19q13.1)
7519	cg43923337	216	GTGGCAGGGAC GACGCCCAAGAT GG[G/gap]AGCTG ACTGATATGGTG GTGTGGGT	G	gap	Ser (9690)	Glu	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14

7520	cg43299409	279	TCGGCCACCAC GGCGCTGAGGA CGC[C/gap]ACGG ATGCCCTCCGTG CCTTCCATC	C	gap	Thr	Arg (9691)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31282 DELTA-6 FATTY ACID DESATURASE - HOMO SAPIENS (HUMAN), 445 aa.	7.9E-181	
7521	cg43951707	415	GCAGCGGCCT TGGCCGAGCGG GCG[G/gap]CCGG GGCTGCAGCC CAAGAAGCGT	G	gap	Ala	Pro (9692)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15814 COFACTOR C - HOMO SAPIENS (HUMAN), 346 aa.	2.7E-178	6
7522	cg43961139	1782	CAAAGGTGTAGA GCTGCTTCCCTT C[G/gap]TGTCGC TTCCCAATGACG GGCATGA	G	gap	His	Gln (9693)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43360 HYPOTHETICAL 98.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	2.7E-178	22
7523	cg43969747	1720	GCATTACCTGG GAGTCCTGGTGC TIG[gap]CACCGT CCGGGTGCAGA TGCCGCTG	G	gap	Gln	Ser (9694)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
7524	cg42733649	1058	AGCCTGGAGCTC CTGTTCCCTGAA TIC[gap]CTTCGG CTTCATCACCTA TCAGGGC	C	gap	Ser	Ser (9695)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-176	
7525	cg42733649	1059	GCCTGGAGCTC CTGTTCCCTGAA TCIC[gap]TTCGG CTTCATCACCTA TCAGGGCT	C	gap	Phe	Ser (9696)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-176	
7526	cg43268525	820	TGTCACCTCCAC AGCTGCCCGCG GA[G/gap]CTGCC ATCGTCACATAC AAATGCAA	G	gap	Leu	Cys (9697)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76815 KIAA0971 PROTEIN - HOMO SAPIENS (HUMAN), 648 aa.	1.1E-176	

7527	cg44035397	1626	TTTTGGTCTGT GGTTTCAGCCGT G[G/gap]CCTGGG CCTAAGGCTCTC CTCTGGC	G	gap	Pro	His (9698)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa.	1.7E-176	7
7528	cg44035397	1632	GTCTGTGGTTTC AGCCGTGGCCT GG[G/gap]CCTAA GGCTCTCCTCTG GCTCCTCA	G	gap	Pro	Pro (9699)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa.	1.7E-176	7
7529	cg43931789	89	CCGAGTCGGCC CAGGGTCCCC GGG[C/gap]CCGG CAGCGTCGCTG GAGCTGTGGC	C	gap	Pro	Arg (9700)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14564 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	2E-175	16
7530	cg43941890	1330	GGCATCAGGAG AAAGCTGGGTC TT[G/gap]GGACC TTGTCTCTCCCA GTTGGCCT	G	gap	Gly	Asp (9701)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	
7531	cg43941890	1332	CATCAGGAGAAA GGCTGGGTCTTG G[G/gap]ACCTTG TCCTCCCCAGTT GGCCTAC	G	gap	Gly	Asp (9702)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	
7532	cg43967532	3773	CACGAGTCGGC CACGGCCTCGC AGA[G/gap]CCAG CGACACGGTA GATGGGCCGG	G	gap	Leu	Ser (9703)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7533	cg43967532	3963	CCATCTTCTTGT AGCCACGTTGT G[G/gap]CACAGC CGCAGGTCCGC GGGGATGT	G	gap	Cys	Cys (9704)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8

7534	cg43967532	4074	GGAAGCTCACGT AGTCGTACTCGC T[G/gap]GCCGAG CCCACGGCCAG AAGCGCCG	G	gap	Ala	Ala (9705)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7535	cg43967532	4128	CCAGCGCCAGC AGCACGCCCGAG GGC[T/gap]GCCC CGCGCGGGCCC CCCTCGGCTGC	T	gap	Ala	Ala (9706)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7536	cg43941339	1446	GTTTAACTGGTA TGGCACAGGTGA T[G/gap]CCTAGG AGGCAAAAGCAA ATCACTG	G	gap	Gly	Gly (9707)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.2E-170	4 (4q21)
7537	cg44032718	794	GCTTCTGGAACC ACAGGTGGCCG AA[G/gap]GGTCT CAAAGGCTCTAA TGGCCTCA	G	gap	Arg	Arg (9708)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.7E-169	X
7538	cg44034179	1178	TGGGCAGAGCC GTTTGGGGCCAC GC[C/gap]ATCGC GGACGTCATCCT GGAGGGTC	C	gap	Gly	Ala (9709)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa.	1.6E-166	4
7539	cg44034179	1272	GGGAAGGCACT AGCTGGGGCTG GGC[C/gap]ACCA GCAGCACCCGG CCCAGGAGCA	C	gap	Val	Val (9710)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa.	1.6E-166	4

7540	cg43926509	1244	CCTGCAGCAGTA ACGGGAGGATG GA[G/gap]GGGCC ACCCCCACATA CAGCGAGG	G	gap	Gly	Gly (9711)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15165 CLONE 22 - HOMO SAPIENS (HUMAN), 306 aa.	4.2E-166	18
7541	cg44003630	1080	ATGGTTGGAATT CGGACCAGATAG A[G/gap]GGCTCG CCCCAGAACATG CCCTCTTG	G	gap	Leu	Ser (9712)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
7542	cg44004690	826	GCTGCTGAGGAT GCTGGAGAAGC GG[C/gap]AGATG GACCGAGCGGA GCACAAAGGG	C	gap	Gln	Arg (9713)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment).	2.5E-161	
7543	cg43929687	425	TGGTGTCTATAAT TCTCCAGCATGA G[C/gap]TCTGCT GGTCCTCTCGGT CTGACCTG	C	gap	Glu	Asp (9714)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa.	8.5E-160	
7544	cg43315424	341	GCTCAGGAACAC CAGGCTGACCG GA[G/gap]GCAGT GCCAGGAGAG GCAGGCTAG	G	gap	Ala	Ala (9715)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q80525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
7545	cg43315424	342	CTCAGGAACAC ACGCTGACCGG AG[G/gap]CAGTG GCCAGGAGAGG CAGGCTAGG	G	gap	Ala	Ala (9716)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q80525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
7546	cg43287561	468	ACTGTGCTCTGG AAGTTGGCATCA A[T/gap]GAAGAT GGGCTCTGCCG CTGTGATT	T	gap	Ile	Leu (9717)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156 9 (9q34)	



7547	cg43287561	553	GTTCCCTTCTGG ATTGTTCTCAGG G[gap/G]ACAAA GGCTGCCCTGGTT TCTGTCA	gap	G	Val	Val (9718)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (human), 300 aa.	1.4E-156	9 (9q34)
7548	cg43298828	702	CCACTCAACTGG CTGGACACCATC A[C/gap]CTGGAT GGTGGTGACCAT GGGCAGC	C	gap	Val	End (9719)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.1E-155	17
7549	cg43288828	703	CACTCAACTGGC TGGACACCATCA C[C/gap]TGGATG GTGGTGACCATG GGCAGCT	C	gap	Gln	Gln (9720)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.1E-155	17
7550	cg41629243	891	TCCTTGGCTCC TTCTTGGCCAGC C[G/gap]CCGTGC GGCTTCTCCTC GGGCGTC	G	gap	Arg	Gly (9721)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	7.8E-155 (19p13.3 )	19
7551	cg42713596	380	CTGTTGGCCGAA ATAGGGCTGAAG C[C/gap]TCTTTG GAGCGAGCTCA GAATCTCA	C	gap	Ser	Leu (9722)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23902 ACTIVATION OF SENTRIN/SUMO PROTEIN AOS1 - HOMO SAPIENS (HUMAN), 346 aa.	3.1E-154	
7552	cg43981925	1805	TATACTGGAAGG TCTTGCTACCAA CTT/gap]GCCCCCT GAAGTGGTGCAC CAGAAAC	T	gap	Gln	Arg (9723)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
7553	cg43060941	1196	TTCCCTTTTICA CTAGATGCAGAG T/gap]TTTTTTGA ACTTTAACCTC ATGTT	T	gap	Asn	Thr (9724)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.9E-153	

7554	cg43060941	960	TCTCTGGTGTCA TAGTCAGTTTTT [T/gap]GTCTCTAT TGGGAGTGAAGT CTTTA	T	gap	Lys	Lys (9725)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.9E-153	
7555	cg43990820	1082	GATGTCTGTGTG ACCCAGCTTGAC C[C/gap]TGGCGG ACCCACTAGTGT TGGACAC	C	gap	Arg	Arg (9726)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.3E-150	3
7556	cg43258297	145	ATAGTCCATACA GTGTGGCTACTG C[C/gap]AAGGTC AGGATGGCCAG CAGACCCA	C	gap	Leu	Leu (9727)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa.	3.8E-150	3
7557	cg43918239	576	AAAGGTGCGC AGAGAGCCCCA GCT[G/gap]GGCA CTTGTTAACTCC TGAGGTCCA	G	gap	Pro	Gln (9728)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
7558	cg43919239	578	AGGTGCGGCAG AGAGCCCCAGCT GG[G/gap]CACTT GTAACTCCTGA GGTCCAGT	G	gap	Cys	Cys (9729)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
7559	cg43943351	418	TGGGTGATATG CGGCTCCACAA G[G/gap]TGCTGA GCACCACGTGG CTCTGTTC	G	gap	Pro	Leu (9730)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17

7560	cg43943351	872	AGGTGGTCACTG TCAATGACAAAC G[C/gap]CCCCAG GCCCTTCAGTCG CTGAGCT	C	gap	Ala	Arg (9731)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17
7561	cg43925047	754	GTGTCCATGAAA CGGGAGCCACT GG[C/gap]CCACG GAGCCATCTTCA AAGCCAGT	C	gap	Ala	Pro (9732)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43730 BK390B3.1 (MANIC FRINGE PRECURSOR PROTEIN) - HOMO SAPIENS (HUMAN), 321 aa.	9.4E-150	
7562	cg43946935	793	AGCCTTATTCA GGTTATCTACTT TTT/gap]GGAAAT GCAGGAAGTTCC CACCTTG	T	gap	Gly	Glu (9733)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60671 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa.	1.8E-149	
7563	cg43930377	1451	TACAAAAAGCTA GCATGGCTTCTT T[gap/A]AAAAAAA ACAATATCCCAA ATAAAA	gap	A	Leu	Leu (9734)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
7564	cg43930377	1459	GCTAGCATGGCT TCTTTAAAAAAA [gap/A]CAATATC CCAAATAAAATC AGAGTC	gap	A	Thr	Asn (9735)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
7565	cg43041577	1597	GAATCTCAAAG GTCGTGTAAGAA G[G/gap]CAAGCC GCAACACAAAGT CTAAGTC	G	gap	Ala	Gln (9736)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.7E-148	10
7566	cg43943919	802	TCGTAGACATGC TCTTGTGGGAT GTT/gap]CTTCCG ACAGAGCATGAT ATAGGCC	T	gap	Thr	His (9737)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa.	2.7E-148	X

7567	cg43965796	1698	GTTGACATCACT GTTGATGCTCTG G[G/gap]CCACGC CAGGGTACTGGA TCCTCAT	G	gap	Ala (9738)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
7568	cg43931669	138	GCCGGGGGAGC CGCCATCGGAG CGC[C/gap]AGGG GACAGAGCACA GGAAAGGGAC	C	gap	Arg (9739)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99703 ATAXIN-2 RELATED PROTEIN - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.3E-146	
7569	cg43937734	827	CTGTGTCTTATG ATGGTGGCTCTG C[C/gap]AAGACC ATCCTGAATAAT GGGAAGA	C	gap	Lys	Arg (9740)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
7570	cg43947808	846	CCCTTTCATCCC TATGTGGAAC GT[G/gap]GGTGGC AAGTGGGAGAAA CCATCAG	T	gap	Gly	Val (9741)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34076 CGI-81 PROTEIN - HOMO SAPIENS (HUMAN), 282 aa.	9.8E-146	16
7571	cg43961927	442	CCAGCTCCTCCC GGCGATGGTGG CG[C/gap]CGTTC TTGGCCCTCTTC CCGGTCTG	C	gap	Arg	Arg (9742)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60928 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
7572	cg43946394	247	AATCTGTAGCTT CCGGATACCGTA G[C/gap]CCACGG GCACCAGCTTGG AAGCCCC	C	gap	Gly	Ala (9743)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
7573	cg43946394	586	TACGTGCTGGGT CTGTGGGGCCG TG[G/gap]CCCGG TGGCCAGGCCA GCTCTTCTC	G	gap	Ala	Ala (9744)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19

7574	cg43946394	840	GGAGGATCACG CTGGCGCCGTTT TC[C/gap]TGGCG GGAGGCACCTG CCACAGGCC	C	gap	Gln (9745)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
7575	cg43983449	1418	TGCATGATGGAA ATGAGGCAGGAT G[G/gap]CAGAGC CAGTGCCAGCTG AGAACAC	G	gap	Ala (9746)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
7576	cg44027658	375	GAAGAAAGTGCCCG GTCCACGCACAG C[G/gap]AGGAGC TTCATGATTGTAT CCAAAA	G	gap	Glu (9747)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
7577	cg43999829	1037	AGGTGGTGAC GGCCTGGAGAA GGC[C/gap]ATCT ACAAAGGCCCA GGCAGCGAAG	C	gap	Ile (9748)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)
7578	cg43958563	1417	GAAAGCAGCTGA GATATAGTACAG G[G/gap]CACAAT GTGCTGGGCTC GGGCTCTT	G	gap	Pro (9749)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)

7579	cg43958563	1482	TTGAGAAAGGTGC GGCGGATCCAAA G[C/gap]CCCCCG GGGACTGCGTG TAGCCGCC	gap	Gly	Ala (9750)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
7580	cg43919223	535	CACITTTATCCAG GACAGCTGTCTC TJA[gap]TGAGTG CTCACCCCAACCT GGGGCCC	gap	Tyr	Leu (9751)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa.	1.4E-140	11
7581	cg42921274	649	ACCAGAGTCTTT CAGGAGCCGGG GT[G/gap]CCAAG GCCAGAATGTGG GTAATGAT	gap	Ala	Asp (9752)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD26417 HEMK HOMOLOG - HOMO SAPIENS (HUMAN), 338 aa.	5E-140	
7582	cg43260991	293	CGCCCCAACCC GCCCCATGCCG CGC[gap]GJCCAC AGGGAGCCAGG AGCCTGTGCG	gap	Pro	Arg (9753)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
7583	cg43260991	301	ACCCGCCCCCATG CCGCGCCCCACA GG[G/gap]AGCCA GGAGCCTGTGC GCAGGCCCA	gap	Ser	Ala (9754)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
7584	cg43292703	992	GCCACTCGAGC CAGATGCTTGT GT[gap]GICGGCG GAGGCCGCGCT GGTGTGACT	gap	Asp	Ala (9755)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99618 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 268 aa.	1.7E-139	

7585	cg43305515	1381	CTCAAGCATGTC GGGCCAGGGA AG[C/gap]CGAAG GCGGACATGAC CGGGGCGCA	C	gap	Gly	Ala (9756)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35297 SECRETED APOPTOSIS RELATED PROTEIN 1 - MUS MUSCULUS (MOUSE), 295 aa.	4.4E-139	4
7586	cg43935076	1655	GAACCGAGTCTC TCTTCTCTATTG [T/gap]TTCACCTC ACTGTAGAAGGT CATAA	T	gap	Lys	Asn (9757)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
7587	cg43935076	1697	AGGTCATAAATG CTTCTCTGGTGC T[G/gap]CCTCCG CCGCCTGAAAGTC CCGCTCT	G	gap	Gly	Gly (9758)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-138	1
7588	cg43952219	1075	CAGTTTGCCAAA GAGCTCTACCAG A[T/gap]TTTTTTG GAGGCATAACAA TAGAAG	T	gap	Asn	Ile (9759)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
7589	cg43952219	1081	GCCAAAGAGCTC TACCAGATTTTT [T/gap]GGAGGCA TAACAATAGAAG TATTGA	T	gap	Pro	Pro (9760)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
7590	cg43994220	232	GCGGGCACCAG GTTGCTCTGGAA GA[G/gap]CTTGA GGATGTGGTCT CGATCACC	G	gap	Leu	Ser (9761)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
7591	cg43994220	282	CTGTTGCACCTT CCGGTATCCCAG G[G/gap]CCACGG CAAGGTCCATCG GGGTGTA	G	gap	Ala	Ala (9762)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19

7592	cg43994220	787	TGGTGGAGTGCT TCAGGGAGCTG CC[gap]TJCCTGT GGAGAGGAAAC ACTGGCATC	gap	T	Gly	Arg (9763)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
7593	cg43929878	1026	CCTGACTGAGGT GGACCGGCAGG GG[G/gap]CCCAC ATTGTTGGCTAC TTCTCCAA	G	gap	Ala	Pro (9764)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O02193 MALES- ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-) - Drosophila melanogaster (Fruit fly), 827 aa.	3.1E-134	
7594	cg43942432	530	AATGAGATTCTC CCAGCAACGGG AG[G/gap]CCAAG CCCTCCGCAGC CGAATAAT	G	gap	Ala	Ala (9765)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.3E-134	2
7595	cg43942432	802	AAGTGTAGTTGT ACTGCAGGGGAT G[C/gap]TCTGCC GGCCAGGGAC AACAGCCT	C	gap	Glu	Asp (9766)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.3E-134	2
7596	cg43916993	1557	CAGGCTGTAAGC TCGCTGCAGATT G[G/gap]CGATGG CCTCATCATAGC TCTCCAT	G	gap	Ala	Ala (9767)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
7597	cg43916679	516	GTGAGCTGTACC TGCGGAGGAAC CG[C/gap]ATCCC CAGCCTGGCTGA GCTCTTCT	C	gap	Ile	Ser (9768)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
7598	cg43916679	845	CTGGACAGCGA GGAGGAGGCAA CCA[G/gap]CGGC GCCCAGGATGAA CGTGGCCTG	G	gap	Ser	Thr (9769)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21



7599	cg43931621	2141	TGGATTCTCCCA CAAAGCCCCGCCA G[G/gap]AGGGAG CCCACGCCCCAG GGTCGCAC	G	gap	Leu (9770)	Leu	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
7600	cg44007142	941	CCAGGCTGGCG TCGCTCTCTGTG TT[C/gap]CCGCT GCCGGGACTTA GCCGCCTTC	C	gap	Glu	Asn (9771)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34089 CGI-94 PROTEIN - HOMO SAPIENS (HUMAN), 253 aa.	3.1E-129	
7601	cg43950545	766	CTGCTACGAATT GTTTGGCGTAG G[C/gap]ACATCT CCTTGCCCCCTCT AGCTTTT	C	gap	Val	Val (9772)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	3.5E-129	13
7602	cg43972431	1944	GGGAGGGAGAT GGCATTTTTGTAG CA[C/gap]CCGGG GAGGGCGTTTCT GTGAACAC	C	gap	Val	Cys (9773)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa.	7.1E-129	2
7603	cg43300586	252	AGTGGCTGCGG CGGGAAGATGG CGG[A/gap]GCTG CGCGTGCTCGTA GCTGTCAAG	A	gap	Glu	Gly (9774)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa.	3.6E-128 (19q13.3 )	19
7604	cg43054809	335	TTGCTCTTGGCT TTTGTGGCCTTG G[C/gap]ATCCAG CGTGCTCTGGG CATGAGTG	C	gap	Ala	Pro (9775)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15125 PHENYLALKYLAMINE BINDING PROTEIN - HOMO SAPIENS (HUMAN), 230 aa.	2E-127	X
7605	cg42891437	229	TTGAGCACGGAG CTCAGGTCCGGA G[G/gap]AACACC ATGGTGAGGAG GCCCAAGA	G	gap	Phe	Phe (9776)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3, SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127 7 (7q21)	

7606	cg43926784	933	GATTGGACCAA TGGACCAGCCAA G[C/gap]TTCCAG CCAGTTACACTG AAAGTCT	C	gap	Lys	Asn (9777)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa.	6.7E-127	
7607	cg43949061	149	GGAGCACCTTG GCCCTGGTCTTG GG[C/gap]CAGCA GACGCAGAAGC AGGGAGTGC	C	gap	Ala	Pro (9778)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7608	cg43949061	150	GAGCACCTTGGC CCTGGTCTTGGG C[C/gap]AGCAGA CGCAGAAGCAG GGAGTGCA	C	gap	Leu	Leu (9779)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7609	cg43949061	178	CAGACGCAGAA GCAGGGAGTGC AGA[G/gap]CCCG GCAACACAGGTGT GTAGCCCCAG	G	gap	Ala	Val (9780)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19

7610	cg43949061	207	GGCAAACAGGT GTGTAGCCCCAG GCG[G/gap]CTCA GATGCAGGTAAT CATACATGT	G	gap	Ser (9781)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7611	cg43949061	390	GATGTTGGCCTC GCGGAAGCAGG CC[C/gap]AGCAC CACAAACCCGGG CCTGGGGCT	C	gap	Leu (9782)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7612	cg43975901	1076	AGCTAATGTGAA CCCTGGAGGAT GG[G/gap]CACCA GCCTCAGTGTTA AGGGCAGT	G	gap	Ala (9783)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa.	2.6E-125	
7613	cg43066224	733	CGGGAGGCTCC CACTGCACCTGT AG[G/gap]TGGCG CTCAGCGAGGG GGCTTAGGC	G	gap	His (9784)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14213 CYTOKINE RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 229 aa.	5.4E-125	19
7614	cg44002548	981	TGATGCATCAGG ACAGGGCTTTTG C[C/gap]ACTGCA CGCTTGAATTC TCCGGAC	C	gap	Thr (9785)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17
7615	cg44002548	1044	GTACCCCTCTCAA CGATCCAGAAAGT T[G/gap]CCACGG CTGCTAGTTGCG TCATCCA	G	gap	Pro (9786)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17

7616	cg43934053	680	TTGGCACCTTCG GGCAAGGGGAG GG[G/gap]CTTGC AGCACCCCCAC CAGTAGGT	G	gap	Gly	Ala (9787)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD39005 RIP-LIKE KINASE - HOMO SAPIENS (HUMAN), 518 aa.	2E-120	
7617	cg43923128	2174	GAGTGGAGATG GGCAGAGGCTC TGG[C/gap]CCCT GCTCCTCTGGCT TCTCAGCAG	C	gap	Gly	Gly (9788)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
7618	cg43963595	156	TCACACTCTCAC ACACACACACAC A[gap/C]TGCCAC GCACATATCCAA GCTCCAA	gap	C	Met	Ser (9789)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
7619	cg43950398	1454	CTGCTTGGTGGC GGCTCGTGAAG GG[G/gap]CAAGG CCGAGAACTTC TGAATGTT	G	gap	Ala	Ala (9790)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
7620	cg43994051	517	AATCTGCAAAG AACATGGCTTTG C[C/gap]GGATGG TTTGAAACCTCT GCAAAGG	C	gap	Gly	Asp (9791)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13637 RAS- RELATED PROTEIN RAB-32 - Homo sapiens (Human), 225 aa.	9.7E-119	6
7621	cg43998873	188	CTCTCAGAATTC CTGACTGTCCGC A[gap]GTTTCC AAATCCTCCAGC GCTTGAG	G	gap	Thr	Thr (9792)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB39895 GRIP1 PROTEIN - HOMO SAPIENS (HUMAN), 849 aa (fragment).	2E-118	

7622	cg43917206	972	GGACCAACAGG CAATATCAATCTT C[C/gap]TCCGGG CTTTAACTGATC TATTAGC	C	gap	Gly	Glu (9793)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P22061 PROTEIN-L- ISOASPARTATE(D-ASPARTATE) O- METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE) (L ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) - Homo sapiens (Human), 226 aa.	6.9E-118	6
7623	cg43258389	1431	GCCACTTCTGCA GCCTGCCGTGT GG[C/gap]AAACT GGATGAAAGCAC ACTGCTGT	C	gap	Ala	Pro (9794)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa.	1.6E-115	5
7624	cg43951899	460	GCAGGCGGTGA GCTGGGGGCCG GCA[G/gap]GGGC GCGGACAGTGC GGCGTGGTCG	G	gap	Leu	Cys (9795)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
7625	cg43951899	463	GGCGGTGAGCT GGGGGCCGGCA GGG[G/gap]CGC GGACAGTGC GG CGTGGTCGAAC	G	gap	Pro	Pro (9796)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
7626	cg43939521	1019	GTGAGCATGACC CCCATGTGCTCC T[G/gap]GCCGTG GCCAAGCTGTTT TGGAGTC	G	gap	Ala	Pro (9797)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	
7627	cg43939521	588	AGCCCAAGATCT GTGCGAGGAGG CC[C/gap]TGCGG CACTATGAGGAC TTCCCCAA	C	gap	Leu	Cys (9798)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	

7628	cg43982971	501	GCGCCATTGAGT TCGGACAGCGG ATG/gap]CTCCA GGTGGCATCTCA AGCCTCCA	gap	Leu	Ser (9799)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7629	cg43982971	742	GCCCTACCTGG GCCCATGGAACC TTC/gap]CCGGTC AGCGGCCCCGA TGTCCTCCCT	gap	Pro	Pro (9800)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7630	cg43982971	744	CCTACCTGGGC CCATGGAACCTC C/C/gap]GGTCAG CGGCCCCGATG TCCCTCC	gap	Gly	Val (9801)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7631	cg43948724	1060	GGAGGAGGCCT GTCCCAATTCTG CC/C/gap]GCTCC ATGGAAGCGG GCTTGACT	gap	Pro	Arg (9802)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7632	cg43948724	1165	TTAATCCTTCTT GTAATACTTCTT A/gap]ATGTGACA TTTCTCTTCCCC TTAGA	gap	End	Tyr (9803)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7633	cg43948724	1166	TAATCCTTCTTGA TAATACTTCTA A/gap]TGTGACAT TTCTCTTCCCCT TAGAA	gap	Cys	Val (9804)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)

7634	cg43948724	1471	TGGAAGCATGTA GACTGTGCCAGA G[G/gap]CCAGAC CCACGGGCTCAT GCACCCC	G	gap	Gly	Ala (9805)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7635	cg43948724	1502	CCACGGGCTC ATGCACCCCTGA GC[C/gap]AGCAG GGCATCTTGGAA AAGGAACT	C	gap	Gln	Ser (9806)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7636	cg43948724	800	CTGATGAGAGAC AGCGCATGCTG GT[gap/C]GCAGC GTAAGGACGAAC TCCTCCAG	gap	C	Cys	Ser (9807)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7637	cg43948724	948	TGCGTCGAAGGA TGCTGGCTGCC GC[C/gap]GCGGA ACGGAGGCTTCA GAAGCAGC	C	gap	Pro	Arg (9808)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7638	cg43921344	959	GGGCCCTCGAAT GGTAAGAGGGG CT[G/gap]CCTGG GGGCCCATGGG TCTGGTAGA	G	gap	Gly	Gly (9809)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7639	cg43921344	108	AGGCCAAGTGG GGAAGTGCAGG TGC[A/gap]CAAG AGAGCGCTTGAG GCTCTGGTC	A	gap	Val	Gly (9810)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	

7640	cg43921344	228	CAGGGCACCGT GCACCATGGGCT GG[C/gap]CCCTC TCGGTGGGAA GTAGCGTGC	C	gap	Gly	Ala (9811)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7641	cg43921344	398	CTAGCGGGGG CAGTATGGGA GAG[C/gap]CCCT CCACGCAGCTG GCATTGATGT	C	gap	Gly	Gly (9812)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7642	cg43957889	325	GGGAGATGGTT GTGGCGGCTTTG C[C/gap]TGCTCC AAGAATGCGCTT TGCCTC	C	gap	Cys	Ala (9813)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
7643	cg43960984	777	ATCTTTTCCCAT CGACCTGGAGTC C[C/gap]TCCTGG GAACCTTAACCAT ACTTCT	C	gap	Gly	Gly (9814)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q61712 DNAJ PROTEIN HOMOLOG MTJ1 - Mus musculus (Mouse), 552 aa.	8.6E-111	10
7644	cg43986282	298	AGAGCCCCTGCT CCTTGGCCATAG C[C/gap]AAATCC CTTGGGCCCAA GTTCTT	C	gap	Gly	Ala (9815)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12
7645	cg43081416	385	CTGGATCCACGC CCCTGGCCCCG AG[G/gap]TCCTG CAGGTCTTCGGG CCGCCCGT	G	gap	Asp	Asp (9816)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45561 TRANSFERRIN RECEPTOR 2 ALPHA - HOMO SAPIENS (HUMAN), 801 aa.	1E-109	7
7646	cg43976845	137	GGGAGCGGCTG GGATGGCGCGT CCG[C/gap]GGCC CCGCCAGTACAA AGCGGGCGGA	C	gap	Arg	Gly (9817)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34137 CGI-142 PROTEIN - HOMO SAPIENS (HUMAN), 203 aa.	3.4E-109	15



7647	cg43928772	1735	ACTAAAGGCGCT TTCCGCCATCAC C[C/gap]CCACTG GCATCTTCGCGG CCGGCCT	C	gap	Gly (9818)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
7648	cg44913737	179	GGCAGGGGCAC TCAGTCCCTCCG CA[G/gap]GTTCT TAAGCCGTTCT CCAGGTCT	G	gap	Leu (9819)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7649	cg44913737	229	TGCATCAGCATC AGCTAGGGCTGA G[G/gap]CTGCGG CCTCTGCTTTTT CCCACC	G	gap	Ala (9820)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7650	cg44913737	237	CATCAGCTAGGG CTGAGGCTGCG GC[C/gap]TCTGC TTTTTCCACC AGCAGCCA	C	gap	Glu (9821)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7651	cg43327495	1079	CTGAAAAGGTGT GATCAATTCCAA CTT/gap]GCACGG CGGCGGTGGTG AGGACGCA	T	gap	Arg (9822)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
7652	cg42657906	195	TCATCAGGTGCT GAGGGGCCCGG GG[G/gap]CGCTG GGGGCAAAAGGC AGAGTAGAG	G	gap	Pro (9823)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11

7653	cg42657906	431	GCCGCCCGCTGC CTGGCTTCCGGC CC[C/gap]TCCGG GCGCCCTTGTC CCATCCAT	C	gap	Arg (9824)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11
7654	cg43296554	206	TGGCCTTCTCTC TTGGGGGCTTTG C[gap/C]TTCTCAT CCTCTTTGTCTG TCAAAA	gap	C	Lys (9825)	Asn	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa.	6.4E-108	9
7655	cg43942004	740	ATGGAGAGAGGT GTCATGGGCTGA G[C/gap]CTCCCA GTGGAATAATCGC TTATATA	C	gap	Ser (9826)	Leu	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
7656	cg43942004	741	TGGAGAGAGGT GTCATGGGCTGA GC[C/gap]TCCCA GTGGAATAATCGC TTATATA	C	gap	Ser (9827)	Leu	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
7657	cg43947512	344	AAGTCAGGTTCC ATTGGCAACTG C[C/gap]GAGTGG ATCGCGGAGCC CGTGGGGC	C	gap	Ser (9828)	Glu	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.1E-107	17
7658	cg42854459	95	AAAAACTATATG AGAAAGCTGGCA A[G/gap]CCCAGT GAACCTCCTGGC CGGAGAG	G	gap	Gly (9829)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa.	3.5E-107	

7659	cg42923937	901	GCTGAGCATTG CCTGTGGTCACG C[C/gap]TTTGAT GAGACGGACGA GGACAGGA	C	gap	Arg	Ser (9830)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment).	4.4E-107	
7660	cg43967668	248	CGCTTGTCGAAC CACTTGCCGTTG G[C/gap]CGCGCC TGACAGGACCG CGCAGTTC	C	gap	Ala	Pro (9831)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
7661	cg43969137	346	GGCTCATAGAAG ATGTGGCTGGTA G[C/gap]CTGCC TGGCCTAGGCC GCAGGAGA	C	gap	Ala	Leu (9832)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O08973 HYPOTHETICAL 33.5 KD PROTEIN - MUS MUSCULUS (MOUSE), 300 aa.	3.6E-105	17
7662	cg43981269	595	ACTCTCCACG CCGAGGCGCAG GC[C/gap]GCCAT CAACGCGCTACA CGGCAGCC	C	gap	Ala	Pro (9833)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	4.5E-105	
7663	cg44912062	504	AGCTGGCCGAG CTGGAGGGCCG CCA[G/gap]GAGG AGCTGCTGGG GAGAACCTAG	G	gap	Glu	Arg (9834)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
7664	cg43989798	491	GCGACTATCTGC TGCGCGGTTACC G[C/gap]ATGCTG GGCGAGACGTG TGCGGACT	C	gap	Met	Cys (9835)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 199 aa.	1.4E-103	

7665	cg43999798	654	CTCCCAAGCTCG GGAGCACCAGC TG[G/gap]CCTCA GCCTCAGAGCTC CCCCTGGG	G	gap	Ala	Pro (9836)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 199 aa.	1.4E-103	
7666	cg43947566	547	GCCTCGACACAA TTACCACAAAAGT G[G/gap]CTCCCC TGGTGCAGTCCT TGTGTGC	G	gap	Ala	Leu (9837)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60427 BC269730_2 - HOMO SAPIENS (HUMAN), 444 aa.	2.9E-103	11
7667	cg43250166	254	AGAGACCCGGC TCGGCTTCATG GC[C/gap]GGCCT CCCGCAGGTGT CTGCCCAGC	C	gap	Gly	Ala (9838)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa.	3.3E-102	2
7668	cg42885795	440	TAAGATGCTGTT TTCTGGCGCTCG G[C/gap]AAAATC ATAGACCACACAGG GATCACC	C	gap	Gly	Ala (9839)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88310 INTELECTIN - MUS MUSCULUS (MOUSE), 313 aa.	4.2E-102	
7669	cg44032186	1169	TTCGGTCGTGAT GCCCTTCATGGT G[G/gap]CCTGCG TGCCCACTGGCA TGAACAC	G	gap	Ala	Ala (9840)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q23623 PUTATIVE QUEUINE TRNA- RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) - Caenorhabditis elegans, 400 aa.	8.8E-102	19
7670	cg43999564	760	CCTTCTGGCTCA GTACGCGGGAC TG[G/gap]CGTAG CGCTCCTCGGCA CTCATCGC	G	gap	Arg	Arg (9841)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15

7671	cg44911139	757	AACTCACGTCGT TCTAAGGGCATT G[C/gap]CTACGT GGAATTCTGTGA AATCCAG	C	gap	Ala (9842)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.9E-101	14
7672	cg44911139	758	ACTCACGTCGTT CTAAGGGCATTG C[C/gap]TACGTG GAATTCTGTGA ATCCAGT	C	gap	Tyr (9843)	Tyr	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.9E-101	14
7673	cg43941552	653	ACTTCCAGATGG AATGCTCTCTGC A[G/gap]GCCAAG CCCGCAGTGCCT ACGTCTA	G	gap	Ala (9844)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	
7674	cg43925214	916	GCGTGAAGGCG TTGGAGTCGAAG GA[G/gap]CGGG ATCCGCCAGCAT CTGGAAGC	G	gap	Arg (9845)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10
7675	cg43941550	531	CACCTCGCCACA CAGGGTGCTCAC G[G/gap]CCATGC CCAGGAAGGCC GGGTCCCC	G	gap	Ala (9846)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)

7676	cg43941550	553	ACGGCCATGCC CAGGAAGCCCG GGT[C/gap]CCCT CCGAGGGTGC TGAGCCTGCA	C	gap	Asp	Thr (9847)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7677	cg43941550	556	GCCATGCCCAG GAAGCCCGGT CCC[C/gap]TCCG GAGGGTCTGA GCCTGCATCT	C	gap	Gly	Gly (9848)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7678	cg43941550	629	TAGACGTAGGCA CTGCGGGCTTG GC[C/gap]TGCAG AGAGCATTCAT CTGGAAGT	C	gap	Gln	Gln (9849)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7679	cg43941550	632	ACGTAGGCACTG CGGGCTTGGCC TG[C/gap]AGAGA GCATTCATCTG GAAGTTGT	C	gap	Leu	Leu (9850)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)

7680	cg43941550	649	TTGGCCTGCAGAG GAGCATTCATC T[G/gap]GAAGTT GTGGACTTTTCT AGTGAGA	G	gap	Gln	Arg (9851)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7681	cg43941550	729	TATCTTCATGAT GTAGCAGCAGGT G[C/gap]CAGGGG CTGGCTTGTAGG CGATCAG	C	gap	Gly	Ala (9852)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7682	cg43950149	925	TCACCTTCTACTG TGGCAAAATTTC C[G/gap]CCTTCA CAGGCCCTTTCT TCATAGG	G	gap	Gly	Gly (9853)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7683	cg43950149	508	GCCAGATCTCAT TGCGCCGTCCTG A[G/gap]GGCTTC ATGGGAGGGTC ATAACCCG	G	gap	Pro	Pro (9854)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7684	cg43950149	560	GCAGAAAGTAGAT GTCCCCCGGTA G[G/gap]TGGCTG TGCCCTCCAGG GCAGCACG	G	gap	Thr	Thr (9855)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7685	cg43926315	2128	GAAGGTGGTGCT GGTGGTGCAACT G[C/gap]TGGTTT TGGAGACAGTAC TGGAAATT	C	gap	Ala	Gln (9856)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42873 NY-REN-37 ANTIGEN - HOMO SAPIENS (HUMAN), 173 aa (fragment).	1.2E-99	14

7686	cg43961133	416	GTGGTGGCCCT GATGCCCGAGG TGG[G/gap]CAGC CTGCAGCACGCA CGGGTGCTG	G	gap	Gly	Ala (9857)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1 - HOMO SAPIENS (HUMAN), 358 aa.	1.5E-99	20
7687	cg44026061	511	ACATGACCTGGC AGCGGGGCCGG AG[G/gap]AGCTT CATCTTCAAGGG CCAGGAGG	G	gap	Ser	Ala (9858)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment).	2.7E-97	
7688	cg43935925	788	TGACCAGGGTCC GGATTTCGTCTG C[C/gap]TTCGGG ATGTTGCTGAA GCAATGAT	C	gap	Lys	Lys (9859)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-98	16
7689	cg43992729	691	CTCCACACTGCT GCAAGGCTCG GC[C/gap]ATATG TTGCTGGGAATT CCCTCCAC	C	gap	His	Ile (9860)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa.	2.6E-95	14
7690	cg43927693	514	GCAGCTGGCCC TGAAGTGGGCAT GG[C/gap]CCCCC ATCTCTTTGGT GCCCCGACA	C	gap	Pro	Pro (9861)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7691	cg43927693	545	ATCTCTTTGGT GCCCCGACAAATG G[G/gap]CTGGGC CTTGGTGGATCT CCTGCTG	G	gap	Gly	Ala (9862)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22



7692	cg43927693	552	TTGGTGCCCGAC AAATGGGCTGG GC[C/gap]TTGGT GGATCTCCTGCT GGTCAGTG	C	gap	Leu	Trp (9863)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7693	cg43927693	723	ACAACCATGGCT GGCGTGGGGA CG[G/gap]CGGCT GCCAGAGTGAGT GCCCCGCC	G	gap	Arg	Gly (9864)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7694	cg43934685	664	TGAAATATTGA TGTCAGTGAAGA G[C/gap]TTCCAG CCAGAGAGAAAT GAAATCG	C	gap	Leu	Phe (9865)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	1.2E-94	17
7695	cg43950632	723	CTGCACAGATGG CGGCTATCAGGC C[C/gap]TTCCGG TTTCCTGCTCC TTCAGTA	C	gap	Lys	Lys (9866)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
7696	cg43993152	1185	GACCCAGACCA GATTTCAACACA TG[G/gap]TTCCC ATACAGGAAGGA CTGCTCTG	G	gap	Asn	Asn (9867)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	
7697	cg42514925	538	CAAGGAACCCAA CAGTCTGCATGG A[A/gap]GGAGTC AGAGGGTTTGAT AAAGTGC	A	gap	Arg	Gly (9868)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12915 IBD1 - HOMO SAPIENS (HUMAN), 204 aa (fragment).	2.3E-93	
7698	cg17948203	321	AGTTACAAGAGT AGTAGATGAACA A[C/gap]ACTAAA GGCGTTGCTTGA GTCCATG	C	gap	Thr	Asn (9869)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75660 DJ501N12.1 - HOMO SAPIENS (HUMAN), 247 aa (fragment).	3.8E-93	

7699	cg42907594	624	GGGAGCATCCC AAAGCATACTCG AA[G/gap]GCTCC AGCCCAGGCAC ATGCCACAA	G	gap	Leu	Phe (9870)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa.	3.8E-92	17
7700	cg43980242	952	GAGAAACTGGG CCTGACCCCGGAT TC[G/gap]GGACA GGAACCTGGTATG TGCAGCCCC	G	gap	Arg	Arg (9871)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
7701	cg43930979	1216	GCCACCATGGG CCTGGCTGGAA GAG[C/gap]CAGA GTGAAGGAAAAA TTTTCCCT	C	gap	Ala	Ala (9872)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPG/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa.	3.4E-90	9
7702	cg43930979	362	CTACGTGCTGTT CCTCGCCGACG AG[G/gap]AGTTC GACGTGGTAGTG TGCGACCA	G	gap	Glu	Ser (9873)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPG/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa.	3.4E-90	9
7703	cg43963913	812	GGAGTCCACAAA CTCGTCACTCAT C[C/gap]TCCGGA GCTCGCGGCCA TAGCGCTG	C	gap	Arg	Arg (9874)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
7704	cg43963913	925	CCATCCCTTCGT CGTCCTCCGTC C[C/gap]GCCGGG TAGGAGCTGTGG CGACTCC	C	gap	Ala	Ala (9875)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11

7705	cg43983527	1032	CGAGAGTCTGC GGCCCCGGTGC TCC[G/gap]GCTG CGATGAGATAAT ATTGCTGA	G	gap	Gly	Ala (9876)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7706	cg43983527	1033	GAGAGTCTGCG GCCCGGTGCT CCG[G/gap]CTGC GATGAGATAATA TTCGCTGAG	G	gap	Gly	Ala (9877)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7707	cg43983527	837	CAAAGAGTGGA ATACGTCGCGA G[C/gap]TCTGCA AGGAGCGGCC CCTCCTGA	C	gap	Leu	Ser (9878)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7708	cg38719198	543	GCAGCAGGCGG ACGTGGTCGTG GCA[gap]A/GAAG TGACACAGCCAT CCTTGGGTG	gap	A	Glu	Arg (9879)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43598 RCL (RCL) - HOMO SAPIENS (HUMAN), 174 aa.	1.3E-89	6
7709	cg43990642	625	CAGGCAGCATT AAACTTAAGCAG A[gap]A/GAGCTT AAAGCAGCGCCT GGGTAAAG	gap	A	Glu	Glu (9880)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
7710	cg43950029	266	TTAGTTGTGTC TGCTAGGCTCTG C[C/gap]TCAGGG ATTTTGGAGTT CTTCTGG	C	gap	Arg	Ser (9881)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q17474 B0334.3A - CAENORHABDITIS ELEGANS, 623 aa.	3.9E-89	
7711	cg44927780	1406	ATAGAGAGGAAA CAACTTGAGGGA G[C/gap]TGGGCG CCATCAATGCAG AGTGCTG	C	gap	Ser	Thr (9882)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23368 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa.	6.3E-89	4

7712	cg44927780	1544	AACGGACCGATC CACAGCCATGTT T[G/gap]CCAGAA GGCAGATGGCA GCTTGATC	G	gap	Ala	Glu (9883)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23368 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa.	6.3E-89	4
7713	cg43059113	425	CAAGAGGGCTG GCATTCTGGCT GG[C/gap]CCTGG GCACTCAGCAGT GCGTGCTT	C	gap	Gly	Gly (9884)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
7714	cg43059113	747	AACAGCAGAGTT TTCACCTCCAGT G[G/gap]CTGGAG CCTGTGATTCAA AGAAAGTC	G	gap	Ala	Ala (9885)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
7715	cg43941586	401	TGGAAGACGGG GATAAGCGCTGT AA[G/gap]CTTCT GCTGGGGATAG GAATTCTGG	G	gap	Leu	Phe (9886)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10589 BONE MARROW STROMAL ANTIGEN 2 (BST-2) - Homo sapiens (Human), 180 aa.	2.5E-88	19
7716	cg43960450	1711	GCTTCAAGATCA GCTCAAAAGCCT G[G/gap]CCAGAG GCACGTTTGTG ATTGCT	G	gap	Gly	Gly (9887)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
7717	cg43026816	65	CAGTCTATGCCT GGCCCAGCGGC AG[C/gap]CCCAG GTCCAGGGGG GTCTGGTTG	C	gap	Ala	Leu (9888)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76103 R29425.1 - HOMO SAPIENS (HUMAN), 656 aa.	2.3E-87	
7718	cg43931874	484	CCTCTGTAATCA TCACTGGCCGCA A[G/gap]GTCCCG GATGTCCTCCTC GATGAGG	G	gap	Leu	Leu (9889)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	

7719	cg43931874	716	TCAGGCGAGCT GGTCCCACCTTG GG[G/gap]CCTTC CCGGCGAATTG GTTACACAGG	G	gap	Gly (9890)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	
7720	cg43296131	436	GAGCTGTCCCTG GTGAGGAACGC CC[C/gap]JAGGCC CCGAGGCACCG GCCCCACGA	C	gap	Gln (9891)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41450 CENTAURIN BETA2 - HOMO SAPIENS (HUMAN), 778 aa.	3.7E-87	
7721	cg43992520	1167	AGCTTCGGGCCCC AGTTTGTAGTAG A[G/gap]GCCGCG CCCCACCTCACC CAGCCCGG	G	gap	Leu (9892)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
7722	cg43946899	371	TTTGGCCGCCA TGTGCTTCCCGA A[G/gap]GTCCTC TCTGATGACATG AAGAAGC	G	gap	Val (9893)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa.	6E-87	
7723	cg43946899	372	TTTGGCCGCCAT GTGCTTCCCGAA G[G/gap]TCCCTCT CTGATGACATGA AGAAGCT	G	gap	Ser (9894)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa.	6E-87	
7724	cg42529218	205	CCCCCGAGGCC AACCCCGCCGA CGG[C/gap]JAGTG ACGCTGACGAG GACGATGAGG	C	gap	Val (9895)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	7.5E-87	
7725	cg43970868	663	ACACCGGGGAC ACTCTGGGCAGC GTC[gap]CTCCG GGGCTTCTTCAC CATCCGCA	C	gap	Leu (9896)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.8E-87	12

7726	cg43918822	3295	ATTGTTCTCCAG GCGTAGCAAGG GG[G/gap]CCACC AGGCCACATTT GTATGGAG	G	gap	Ala (9897)	Ala (9897)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
7727	cg44018226	1715	AGGCTCCCAGG CTCCAGGAGCC GGG[G/gap]CTGA CGCTTGTCACCC ACCAGGTAC	G	gap	Pro (9898)	Pro (9898)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
7728	cg44920099	591	TCTCCAGTCCCC ACCACCACGATC T[C/gap]TATCCG GGGCTCCAGCA ACCAGAAG	C	gap	Glu (9899)	Arg (9899)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment).	1.7E-86	
7729	cg44920099	772	CGATGTACATTG CCTGAGCGGCC TC[G/gap]CGTTG CAGCAGAGAGAT GCGCGTCC	G	gap	Arg (9900)	Arg (9900)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment).	1.7E-86	
7730	cg43995092	404	ATACTTGCTGA GGGCCCTTGAGG GC[C/gap]GATCA TCCAATCCAGTT GCAGTACT	C	gap	Arg	Asp (9901)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD18134 T41P - HOMO SAPIENS (HUMAN), 505 aa.	1.1E-85	8
7731	cg43934734	931	AACCACCTTTATG TAGGGGCCGGG GA[G/gap]CCCTC CAAGGGCATTGA AGCACAGA	G	gap	Leu	Ser (9902)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
7732	cg43934734	670	CGATGGGAGAC AGCGTTCTTCTC CG[C/gap]CTTAG GCATCTCTGCGT ACGTCTGC	C	gap	Ala	Arg (9903)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20

7733	cg44032523	298	GTCCAGGTCGG GACCCTCCCGTA CG[C/gap]TGTCG TGCAGGTCTTCA GAGGAGCC	C	gap	Ser	Thr (9904)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	9.1E-84	
7734	cg44007579	255	GCACCTCCAGGT GCACAGCGCGG GA[G/gap]CCGTC ACGGTGCTCAAG GCTCCCAA	G	gap	Ala	Pro (9905)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83007 KIAA1055 PROTEIN - HOMO SAPIENS (HUMAN), 868 aa (fragment).	2.2E-82	
7735	cg43967808	127	GGCGATGGGCT TGTAGGGCCGG CGG[G/gap]CAGC ACGCTTGGTTTC CGAGGATGA	G	gap	Ala	Ala (9906)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa.	7.3E-82	14
7736	cg43967808	73	GTTGACGGGCG CAGGTGGCGGT GGC[gap]CJCGG CGGCAGGGCCT GGCTCTGGCG	gap	C	Arg	Arg (9907)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa.	7.3E-82	14
7737	cg43967808	87	GGTGGCGGTGG CGCGGCGGCAG GGC[C/gap]TGGC TCTGGCGCAGG GCGATGGGCT	C	gap	Gln	Gln (9908)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa.	7.3E-82	14
7738	cg43283313	937	CCTGCACGTAGC AGGTGAGCAGC CG[C/gap]GTCCG CTCCCCGGTCAG GAGCGCAG	C	gap	Thr	Thr (9909)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43658 CANDIDATE TUMOR SUPPRESSOR P33ING1 - HOMO SAPIENS (HUMAN), 279 aa.	1.9E-81	4

7739	cg43336199	689	CTCCCGGAGGA GGGCACCGTAG TTA[G/gap]CCTC CTGGCAGGCAG TGGTCATGAA	G	gap	Ala	Val (9910)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
7740	cg44024149	657	GAAGTCAACTGT GTGAGTGTGATA A[G/gap]GCTGCT GCCACCTGTTTT GCTAGAA	G	gap	Ala	Leu (9911)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
7741	cg43250517	354	TCAGCATGGAAA CCTGGGAGAAA GG[C/gap]CTGTT CCTGAAGGTACA GCAGCCGG	C	gap	Ala	Pro (9912)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	1.4E-78	
7742	cg43949675	367	GTGTCCCGTGTC TGAATGCACCGC A[G/gap]GCAGCA CAAGTTCTCATA TCCTTGC	G	gap	Leu	Cys (9913)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
7743	cg43949675	368	TGTCCCGTGTC GAATGCACCGCA G[G/gap]CAGCAC AAGTTCTCATAT CCTTGCT	G	gap	Cys	Cys (9914)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
7744	cg43304219	1236	TCTATCAGCAGA GACAGCTTCTTC TT[G/gap]CAGTTC CTGCAAGTCCCT TGAGATA	G	gap	Gln	Arg (9915)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00323 HYPOTHETICAL 17.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 161 aa.	9.9E-78	16 (16p13.1 1)



7745	cg43936167	690	TTGCAGTCTGTT CCACAGTTTTGG CT[ <i>gap</i> ]TTTTTTC TTTTCTTTTTTCT TTTCT	T	gap	Ser	Ala (9916)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	1.2E-77	20
7746	cg43936167	696	TCTGTTCCACAG TTTTGGCTTTTTT [T/ <i>gap</i> ]CTTTTTCTT TTTTCTTTTTCTTT GTCA	T	gap	Lys	Lys (9917)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	1.2E-77	20
7747	cg44938941	694	CTCGTGTCTCT CATCTGCATCAA A[A/ <i>gap</i> ]TACCAA ACAGTTATTGCG TACCTTG	A	gap	Tyr	Tyr (9918)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
7748	cg43931888	306	CAACGCCGAAC GCCTCCAGGA GG[C/ <i>gap</i> ]CCACC TGGGAACCCCC GACCTGAAC	C	gap	Ala	Ala (9919)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa.	1E-75	22
7749	cg43970034	870	ATTGTGCTGTTC TTCAGGCTTCTT TTT[ <i>gap</i> ]TCTGAGT CAGCATCTTTTC TCTGGC	T	gap	Lys	Lys (9920)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa.	1.3E-75	16
7750	cg43970034	871	TTGTGCTGTTCT TCAGGCTTCTTT TTT[ <i>gap</i> ]CTGAGT CAGCATCTTTTC TCTGGCT	T	gap	Lys	Lys (9921)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa.	1.3E-75	16
7751	cg44924517	65	CGGCTACCAGG AAGAGCTGCCCG AA[G/ <i>gap</i> ]GTGAA GGCCATGGACTT CATCACCT	G	gap	Val	End (9922)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	1.6E-75	

7752	cg42897014	220	ACAAGGACCTCA AAGTCACAGCG A[G/gap]CTTCTC CTGCTGGGCCC CTGCTGCC	G	gap	Leu	Cys (9923)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7753	cg42897014	234	GTACACAGCGCA GCTTCTCCTGCT GC[G/gap]CCCCCT GCTGCCAGGGG GCAAGTGGT	G	gap	Ala	Gly (9924)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7754	cg42897014	449	CGGCCGCTGCG GCCGCCCTTCTGC AC[C/gap]TGCGG GTCGTCGGGCG ACAGGTCCC	C	gap	Gln	Gln (9925)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7755	cg42897014	523	TGCGGCCGGCG CCGGCGCTCGC GTG[G/gap]CAGC GCCAGGAGGCA GAATGCGACC	G	gap	Pro	His (9926)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7756	cg44909359	206	CATAGACGAGG GCAAAGCGGCG TCAIgap/GJCCAA GTTAATCAGATC AACACTGAG	gap	G	Thr	Ser (9927)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa.	4.1E-75	
7757	cg44909359	248	AACACTGAGCGA TGCAATCCGAGA G[G/gap]CAATAG CTGAAGGCCATA TAACAAC	G	gap	Ala	Gln (9928)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa.	4.1E-75	
7758	cg43971400	386	GGAAACATCCT TGTAATGCGACT A[G/gap]CAACCA AGGAACAAGAGA TGCAAGA	G	gap	Ala	Gln (9929)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15007 HYPOTHETICAL PROTEIN KIAA0105 - Homo sapiens (Human), 151 aa.	4.4E-75	6

7759	cg44012742	1302	GGAGCGCAACTA CTGCCGCTGC GG[G/gap]AGGCT CTGCAGCCCCCTG CTTACCCA	G	gap	Glu	Arg (9930)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
7760	cg43272466	1780	CAGTTCTTGGTG GATGCAGTGAAA C[C/gap]TTCGGC CTTTGCTGTGAC CACATAC	C	gap	Gly	Val (9931)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
7761	cg43989639	775	TCATCCCCGGGCA GGAGAGGCTGT GG[C/gap]CACAT ACACCTGATTAT CAACAGCC	C	gap	Ala	Pro (9932)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
7762	cg43989639	776	CATCCCCGGGCA GGAGAGGCTGT GG[C/gap]ACAT ACACCTGATTAT CAACAGCCC	C	gap	Val	Val (9933)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
7763	cg43982490	395	GTCAGCTTCACC ATCATGGGCGAG A[G/gap]CTCATA GAGGACGAAGA CTCCGGGA	G	gap	Leu	Ser (9934)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34049 CGI-54 PROTEIN - HOMO SAPIENS (HUMAN), 383 aa.	1.4E-73	2 (10q21)
7764	cg43981873	641	CCGAGGTGTGTT TGGTGGCCGGG GC[C/gap]GAGGT GGGATCCCCGGG CACAGGCAG	C	gap	Arg	Glu (9935)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
7765	cg43981873	670	GTGGGATCCCG GGCACAGGCAG AGG[C/gap]CAGC CAGAGAAAGAGC CTGGCAGAC	C	gap	Gln	Ser (9936)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	

7766	cg43981873	671	TGGGATCCCG GCACAGGCAGA GGC[C/gap]AGCC AGAGAAGAAGCC TGGCAGACA	C	gap	Gln	Ser (9937)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
7767	cg43933021	645	CTCTGCTGGTCG ACGTCGGCGTCT G[G/gap]CCGTTT GGCCGAGGGCT GCAAGTAC	G	gap	Pro	Gln (9938)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
7768	cg43933021	653	GTCGACGTCGG CGTCTGGCCGTT TG[G/gap]CCGAG GGCTGCAAGTAC TCAGCGTA	G	gap	Ala	Ala (9939)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
7769	cg43271682	164	AGTTCACTGCCC CGCACCTGCGC CC[T/gap]CAGCC CCGCCAGCGC TTCTGCCCGT	T	gap	End	Trp (9940)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
7770	cg43923124	261	TATAGAGGGCTG CTGTATTTCAG A[G/gap]CTAAGT CCTCCAGTTCTC GATTAC	G	gap	Ala	Leu (9941)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	2.9E-70	
7771	cg42696021	457	CACAATGAAGTG AACCGGAAGCTG G[G/gap]CAAGCC TGATTTTGACTG CTCAAGA	G	gap	Gly	Ala (9942)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
7772	cg3003900	333	CGTGCGGGGAGC GGGGGCCCGCTG CGC[G/gap]GTCT TGGGCCTCTGCT GCAGCCCGG	G	gap	Val	Ser (9943)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OCYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa.	1.8E-69	20 (20p13)

7773	cg3003900	334	GTGCGGGAGCG GGGGCCGCTGC GCG[gap]TCCT GGCCTCTGCT GCAGCCCGGA	G	gap	Val	Ser (9944)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OCYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa.	1.8E-69	20 (20p13)
7774	cg42921698	337	CCCCGCCACCT CCACCAGGCGC AC[gap]CGCGC CAGCGGCAGGC GGTGGCGGA	G	gap	Arg	Arg (9945)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7775	cg42921698	472	GGAAAGGAACG CCCGGCCCGCG CTC[gap]TCGC GGCCCCAGGAG CCTTGCTCCT	C	gap	Glu	Glu (9946)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7776	cg42921698	478	GAACGCCCGGC CCGCGCTCCTC GCG[gap]CCCC AGGAGCCTTGCT CCTTGCTGT	G	gap	Gly	Gly (9947)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7777	cg42921698	644	GCCGCGAATTCT CAGCACCCTGC CA[gap]GGCGG ATGCCCTCGGG CAGCGAGGA	G	gap	Pro	Leu (9948)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7778	cg42921698	646	CGCGAATTCTCA GCACCGTGCCA GG[gap]CGGAT GCCCTCGGGCA GCGAGGACT	G	gap	Arg	Arg (9949)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19

7779	cg42921698	652	TTCTCAGCACCG TGCCAGGGCGG AT[G]gap]CCCTC GGCAGCGAGG ACTTGTGGG	G	gap	Gly (9950)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7780	cg43266481	341	CTGAAAGAATAA TTCAATATTATG G[G]gap]CCCAGC CACCTGGGGCA GAAGATGG	G	gap	Pro (9951)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14264 ENVELOPE PROTEIN - HOMO SAPIENS (HUMAN), 564 aa.	5.3E-69	
7781	cg43930848	596	CAACGCGTTCAG GACCCCGGCGC GG[G]gap]CAGGG CGCCACGAGC TGCGTGGCT	G	gap	Ala (9952)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.9E-69	7 (7q21)
7782	cg42925004	580	AGCCACCCTATC TCCATGGCTGTG G[C]gap]CCTTCA GGACTACATGGC CCCCGAC	C	gap	Ala (9953)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa.	1.6E-68	
7783	cg42925004	671	TCCTTCTCCAAGC TGAAGGGCCGT GG[G]gap]CGGCT CTTCTGGGGAG GCAGCGTTC	G	gap	Gly (9954)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa.	1.6E-68	
7784	cg44004331	524	GGCAAAAGCAAA CTTGAGGCGGTA G[G]gap]CCTCGG CCAGCAACAGG CTGATGTC	G	gap	Ala (9955)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	

7785	cg43958562	301	GCATGTTGTCCTT CAGTCTGCTTTG C[A/gap]GCATCT AAAAATTTTCGT GCAGAAA	A	gap	Ala (9956)	Ala	Ala	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33909 COLON CANCER- ASSOCIATED PROTEIN MIC1 - HOMO SAPIENS (HUMAN), 609 aa.	9.1E-68	18 (18q11)
7786	cg42831353	481	GCGGCTCCACA CGTACACCAGCA TG[G/gap]CCATG AGGCCTGGCCC AGGAAGAAC	G	gap	Ala (9957)	Ala	Ala	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.3E-67	22
7787	cg43980385	446	GGCAGGAACCC TCCTTATCATTG GG[gap]GJCAGAG AGCAGAAAGGTG GCACAGCCC	gap	G	Pro (9958)	Pro	Pro	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7788	cg43980385	452	AACCTCCTTAT CATTGGGCAGAG A[gap/A]GCAGAA GGTGGCACAGC CCGCGCTG	gap	A	Phe (9959)	Ser	Ala	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7789	cg43980385	463	ATCATTGGGCAG AGAGCAGAAAGGT GG[gap]CACAGC CCGCGCTGCAG CACTTGAG	G	gap	Ala (9960)	Ala	Ala	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20

7790	cg43980385	469	GGGCAGAGAGC AGAAAGGTGGCA CAG[C/gap]CCGC GCTGCAGCACTT GAGGTTGTC	C	gap	Gly	Ala (9961)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7791	cg43980385	555	AGTTCTGGTCAG CCTGGAGCTCG GG[G/gap]CACAC GCCAGTCTTCTC TGCTCCTG	G	gap	Cys	Cys (9962)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7792	cg43080742	299	AAC TGGGCCCGGT GTGGGAACCTG GC[C/gap]TGCCG GTCAGACCTCCA GGTGGCGG	C	gap	Cys	Ala (9963)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Fig. 541 aa.	2.2E-66	21



7793	cg43080742	324	CTGCCGGTCAGAG CCTCCAGGTGG CG[G/gap]CCAAA GCCCTGGAGAT GGGCGTGTT	gap	Ala	Pro (9964)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53803 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa.	2.2E-66	21
7794	cg44911411	438	GAATCTCGTGAC ATTGGCCACAG C[C/gap]TGAGCA AGACCTGTTCCC CGGCCCTG	gap	Leu	End (9965)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7795	cg44911411	454	GGCCACAGCCT GAGCAAGACCTG TTC[gap]CCCCG CCTGCCCATCC CAGAAAGGC	gap	Ser	Ser (9966)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7796	cg44911411	553	CTGTGCAATTC AGTGGGCCCA TG[G/gap]CGGC TGCGGGCAAGC GTCACCCCTG	gap	Gly	Ala (9967)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7797	cg43294227	351	CAGGCGCGGG CCTGCGGGCCA AGG[G/gap]CCCC GGGGGCACGAG CGACGCGTAC	gap	Gly	Ala (9968)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7798	cg43294227	571	GCCTCGACAAGT TCCTGGGCCGC GC[C/gap]GAGGT GGACCTGCGGG ATCTGCACC	gap	Glu	Arg (9969)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8

7799	cg43294227	612	GATCTGCACCGC GACCAAGGCGCG CA[G/gap]GAAGA CGCAGTGGTATA AGTTGAAA	G	gap	Arg (9970)	Arg (9970)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7800	cg43294227	613	ATCTGCACCGCG ACCAGGCGCGC AG[G/gap]AAGAC GCAGTGGTATAA GTTGAAAT	G	gap	Lys (9971)	Arg (9971)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7801	cg43294227	622	GCGACCAGGGC CGCAGGAAGAC GCA[G/gap]TGGT ATAAGTTGAAAT CCAAACCAG	G	gap	Trp (9972)	Gly (9972)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7802	cg44010741	114	GAGGCGGCGCG GAGCCTGCCCT GG[G/gap]CGCCA GGTGTTCGGG GTGCGGGTC	G	gap	Gly (9973)	Ala (9973)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa.	6.6E-65	5
7803	cg44010741	143	CAGGTGTTTCGG GGTGCGGGTCT CG[C/gap]CGACC GGGGAGAAGGT CACGCACAC	C	gap	Pro (9974)	Arg (9974)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa.	6.6E-65	5
7804	cg42722355	80	TCGCCTCTTTCA TCCTGGCCTTTG G[C/gap]ACCGGA GTGGAGTTCGTG CGCTTTA	C	gap	Thr (9975)	Pro (9975)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45885 MULTISPANNING NUCLEAR ENVELOPE MEMBRANE PROTEIN NURIM - HOMO SAPIENS (HUMAN), 261 aa (fragment).	1.8E-64	

7805	cg44001502	188	AACGCTCTCACC GGGAGCCAGAG CT[C/gap]CCATG CTTCTCTGCGCA ATATCCAT	C	gap	Ser (9976)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
7806	cg43969715	585	GAGCTCGTCATG ATTGGCCAGGTG T[G/gap]CTCTGC AGTGGATACAGC TGTACGT	G	gap	Ala (9977)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60688 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa.	3.3E-63	22
7807	cg40360053	217	TCGCTCACTGGC TCCTCCGGCGG CA[G/gap]CTCGT GCTGAGGGAGC TCCTGGCTG	G	gap	Leu (9978)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O14598 TESTIS-SPECIFIC BASIC PROTEIN Y 1 - Homo sapiens (Human), 125 aa.	8.7E-63	
7808	cg43969918	999	ACGGATGTATAC CTGCTCCAGCTG T[G/gap]CCACTC GGCCATCTCTGT ATGTGAC	G	gap	Ala (9979)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa.	2.9E-62	22
7809	cg44017203	137	GTAGATGCTAGT GGAGGGCGCCC GC[C/gap]TGGCG ACGAGGCAGAG GCAGGCAGC	C	gap	Ser (9980)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	6E-62	11
7810	cg44017203	141	ATGCTAGTGGAG GGCGCCCGCCT GG[C/gap]GACGA GGCAGAGGCAG GCAGCAAGA	C	gap	Pro (9981)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	6E-62	11
7811	cg43950850	465	CAAGATAATATC CAGCAAAAAA A[gap]AGGCCGT AATATATAGAAG CTGGCGA	gap	A	Phe (9982)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11

7812	cg43329229	183	GCCCGTGCAG ATCGGCTGCTGA AA[G/gap]CCCCGT GCCCTGAAGATC CGGGAGGA	G	gap	Ala	Pro (9983)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment).	5.4E-61	
7813	cg43329229	207	AGCCCGTGCCT GAAGATCCGG AG[G/gap]AGCG AGCGTTATGACG ACCGACGA	G	gap	Glu	Ser (9984)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment).	5.4E-61	
7814	cg40157055	196	GGACTGCTCGTG GCCGCGGCGT GG[C/gap]CGCG CTGCGCTCTTGC TGGTCCAC	C	gap	Ala	Ala (9985)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35675 M-DELTA-LIKE 3 GENE PRECURSOR - MUS MUSCULUS (MOUSE), 585 aa.	5.5E-61	
7815	cg43298020	237	TGGTGGATCACC TCAATGTGGTG T[G/gap]GCCCCAG GCCTACATGAAC CAGAGAA	G	gap	Ala	Pro (9986)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7816	cg43298020	238	GGTGGATCACCT CAATGTGGGTGT G[G/gap]CCCCAGG CCTACATGAACC AGAGAAA	G	gap	Ala	Pro (9987)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7817	cg43298020	245	CACCTCAATGTG GGTGTGGCCCA GG[C/gap]CTACA TGAACCAAGAGAA AGCTGGAC	C	gap	Ala	Ala (9988)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7818	cg43285334	613	GATTGCTTCAT TAAACGCTTGGT T[C/gap]CCGTTT CGGTCGTAGGC GGCCCCAGA	C	gap	Gly	Gly (9989)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1

7818	cg43285334	615	TTGTCCTTCATTAA ACGCTTGTTCC [C/gap]GTTCCGG TCGTAGGCGGC CCAGATG	C	gap	Gly (9990)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
7820	cg43985327	248	GGGACCTCAGT GGACACTTCGGT GG[G/gap]CACTG CCAGCCGCGTG GGGGGCACA	G	gap	Pro (9991)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7821	cg43985327	255	CAGTGGACACTT CCGTGGGCACT GC[C/gap]AGCCG CCTGGGGGCA CATAGGATC	C	gap	Leu (9992)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7822	cg43985327	499	CTGGGGTCTGTG CGGATCCCTGAG GC[C/gap]GCAGC TCGCGGTGAATC TCATCCAA	C	gap	Arg (9993)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7823	cg43278994	422	GGCCATACCCCT GCCAGCCGCGA CA[G/gap]CTCCT CTGTCCTCCCGG ACAGCGTG	G	gap	Cys (9994)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment).	3E-59	19
7824	cg43278994	572	GCGGTTCTGTTCA CCTTGCCCGCCA G[G/gap]CAGCAG TGTGATAGGCA TTGTGGA	G	gap	Cys (9995)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment).	3E-59	19
7825	cg43976473	761	TGGGATGCGATG GAGCTGCCATAG G[C/gap]CATAGC CACATTGGCCAT TGGGTCC	C	gap	Pro (9996)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11

7826	cg43939569	807	AGCCTTTTCTAC TATCACCAGGCAC C[C/gap]GGTCCG GGTATTTCTTTC GGATCTT	C	gap	Arg (9997)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
7827	cg44011422	729	GAGAAAGATGCAC GAGGGTGACGA GG[G/gap]CCCTG GCCACCACCCATA AGCCAGGC	G	gap	Gly (9998)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7828	cg44011422	737	GCACGAGGGTG ACGAGGGCCCT GGC[C/gap]ACCA CCATAAGCCAGG CCTCGGGGA	C	gap	Thr (9999)	His	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7829	cg44011422	765	CACCATAAGCCA GGCCTCGGGGA GG[G/gap]CACCC CCTAAGACCACA GTGGCCAA	G	gap	Ala (10000)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7830	cg44937260	130	TCCGAGCACGTC GCCGAGATCGTC G[G/gap]CCGCCA GGTTGTAAAT TAAAGCA	G	gap	Ala (10001)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94140 MEX-3 - CAENORHABDITIS ELEGANS, 415 aa.	4.4E-59	

7831	cg44914411	669	AGGCCCGCTCC GGAGAGCCCCG GAC[C/gap]TGAC GGGTGCCAATAC TAGCCAGCG	C	gap	Arg	Ser (10002)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
7832	cg44915744	243	AAGATTCGAGCG AAATATCCCGAC A[G/gap]GGTTCC GGTGATTGTGGA AAAGGTC	G	gap	Arg	Arg (10003)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa.	1.9E-58	16
7833	cg42717343	380	TCCTACTGATG TTGAGACAGTCT C[C/gap]TCCGGC TTTCTGGAAGAA TTCACTG	C	gap	Ser	Pro (10004)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa.	1.9E-58	
7834	cg43253299	428	GGAAGCTCCTT CTGGACGAATGT C[C/gap]ATCGTT AAGAACCTGCAG AACCTGG	C	gap	Ile	Ser (10005)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06307 PROCHOLECYSTOKININ PRECURSOR (CCK) - Homo sapiens (Human), 115 aa.	4.6E-57	3
7835	cg43962116	616	CTGCAGGTCAAA TAGACAGTCCGA A[G/gap]GCACTG ACGATGCAGTAC ATGGTCT	G	gap	Ala	Ala (10006)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa.	5.9E-57	6
7836	cg43962116	617	TGCAGGTCAAAT AGACAGTCCGAA G[G/gap]CACTGA CGATGCAGTACA TGGTCTT	G	gap	Ala	Ala (10007)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa.	5.9E-57	6

7837	cg43934461	580	GAGGTGGATGC CGGCCCTAGCA CTG[G/gap]CCCT GGCCCTCATACT GGCTTCAGC	G	gap	Ala (10008)	Ala (10008)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa.	8.8E-57	3
7838	cg43919432	1237	CTTGGATTCTG CAGTTCAGTAA C[C/gap]TCCGGC GGCGCTCACTCT GCTCCAA	C	gap	Arg	Ser (10009)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7839	cg43919432	459	TC TTGTGCTCCA TAATCTGCTGGA G[C/gap]TGGTGC CCAGCATAGTCT GGCTTGG	C	gap	Gln	His (10010)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7840	cg43919432	537	CACCAAGGACAT CTGACACCATGT A[G/gap]GGCGC AGCCAGCCAC CAAGGGAG	G	gap	Pro	Pro (10011)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7841	cg43919432	540	CAAGGACATCTG ACACCATGTAGG G[G/gap]CGCAGC CAGCCACCAAG GGAGTGC	G	gap	Arg	Arg (10012)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7842	cg43991184	51	CGGACCTCACCA AGCACCGGCGC AC[G/gap]CACAC GGCGGAGAAGC CCTACCGCT	G	gap	His	Thr (10013)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1



7843	cg43991184	67	CCGGCGCAGCG ACACGGCGGAG AAG[C/gap]CCTA CCGCTGCGAACT GTGCGGCAA	C	gap	Pro	Pro (10014)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7844	cg43991184	69	GGCGCACGCAC ACGGCGGAGAA GCC[C/gap]TACC GCTGCGAACTGT GCGGCAAGC	C	gap	Tyr	Thr (10015)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7845	cg43991184	93	CCTACCGCTGCG AACTGTGCGGCA A[G/gap]CGGTTC ACGTGCGGTGTC AATCTCA	G	gap	Arg	Gly (10016)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7846	cg44011808	666	CACCATCTCCAG CAGTCCGTGCG CA[G/gap]CCGCT TCTGAAAAGCG GCCTCCAA	G	gap	Gly	Gly (10017)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa.	2.5E-56	
7847	cg43999272	171	ATCGCGGACGG AAGATGGCGTCC GC[C/gap]ACCCG TCTCATCCAGCG GCTGCGGA	C	gap	Thr	Pro (10018)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.2E-56	19
7848	cg43999272	290	CAGCCTCCTCCC AAGCTCCCCTGTG G[G/gap]TCCTAG CCACAAGCTCTC CAACAAT	G	gap	Gly	Val (10019)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.2E-56	19

7849	cg42697199	304	ATGTTGATGTAG ACTTTGCCATCT T[C/gap]TTGGGC GGGGCTGCGGC GTGGGCGT	C	gap	Glu	Lys (10020)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43303 HYPOTHETICAL 13.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 131 aa (fragment).	1.1E-55	19
7850	cg43935092	198	GCCTTCAGACCA ACTCCTGGATAT G[gap/G]AGCTCA ACCTTCAACAAG ACTACAC	gap	G	Ser	Glu (10021)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD28982 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.8E-55	2
7851	cg44019498	1102	TAGCCTGTCTAC CATGAAATCAAT G[G/gap]CATCAG CCATCATAGGGT CCACCGG	G	gap	Ala	Ala (10022)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
7852	cg43269198	618	AGCATTGCCATT CCAGACACAGG TG[G/gap]CTGTG CCCATGTACAGG CGGGACAG	G	gap	Ala	Ala (10023)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41301 DJ598C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment).	1.8E-55	20
7853	cg43917989	763	CCCCTCTGGCCA TGGGCATGCTTG CTT/gap]GGGGCC GCCACGGGTGC TGCTCTTG	T	gap	Gly	Gly (10024)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.3E-55	11
7854	cg43916991	719	CCCTTCTTGTC CTGCAGCGTGTG G[G/gap]TCATTTT GACCCCGTGAC CCGGAGC	G	gap	Gly	Val (10025)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
7855	cg43129880	187	CTGGACACTGTG GAAGTGTGAAA G[C/gap]AATTCA GAAAGCCCAAGG GGTCAAG	C	gap	Ala	Glu (10026)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	1.1E-54	3

7856	cg43957773	453	CGTAGAGCAACT GCAATCGCTCTG G[G/gap]CCTGGG CCTGGACAGGA CGGAGACC	G	gap	Ala (10027)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa.	3.3E-54	19
7857	cg43123055	468	AGCTGCAGTCGC TGGTCCCTCAGG G[gap]GJAGGTGT GGGAGAGCTGTC CCCAATGG	gap	G	Ser (10028)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2
7858	cg43123055	495	GGTGTGGGAG CTGTCCCAATG GG[G/gap]ATGGG CTGGAAGGCTCC AGACTCTT	G	gap	Ser (10029)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2
7859	cg43969772	707	CAGATTCGTAGT CAGCATAAGTTC T[G/gap]CCTTCT GGCCTCTTGGTA GGCTGTA	G	gap	Gly (10030)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
7860	cg43969772	728	TTCTGCCCTTCTG GCCTCTTGGTAG G[C/gap]TGTAAC AGCAAAATGGTG TGAGACA	C	gap	His (10031)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
7861	cg43047973	270	CCTGGCGAGCG CTCTGGGCTGGT GC[C/gap]ACCGG GTGATCTCCTAC CGGGGCCA	C	gap	Ala (10032)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q02080 MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2) - Homo sapiens (Human), 365 aa.	1.9E-51	19

7862	cg42903443	120	CGCGGCAGCCA GAGCGCTGGTC CGC[G/gap]CAGG TTGGCCAGCAGC GGCGGCACC	G	gap	Arg	Ala (10033)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45012 573K1.15 (MM17M1-6 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE) PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa (fragment).	1.9E-51	
7863	cg43511776	96	TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG	A	gap	Asn	Thr (10034)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
7864	cg44341684	96	TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG	A	gap	Asn	Thr (10035)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
7865	cg43924435	847	GTAGGACCTTCT GCCACTGGGCA AG[C/gap]TCCGC CTGCCGCATGGA ATGCAGTT	C	gap	Glu	Asp (10036)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20971 HSPC009 - HOMO SAPIENS (HUMAN), 106 aa.	2.8E-50	17
7866	cg44010855	596	CACTGCCTGCAC CCCAAGCTGCAG A[G/gap]CACCAA GCGCTTCATCAA GTGGTAC	G	gap	Ser	Thr (10037)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
7867	cg43298240	375	CAACCAGCAATG AAGGTGAAGATG C[G/gap]GGGGG GGCAGGTCCTCG GGACGGGTT	G	gap	Arg	Ala (10038)	FRAMES HIFT	water_ch annel	Human Gene Similar to SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	4.9E-65	

**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide selected from the group consisting of:
  - a) a nucleotide sequence comprising one or more polymorphic sequences  
5 selected from the group consisting of SEQ ID NOS:1 - 7867;
  - b) a fragment of said nucleotide sequence, provided that the fragment  
includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence  
10 complementary to one or more of said polymorphic sequences selected  
from the group consisting of SEQ ID NOS:1-7867; and
  - d) a fragment of said complementary nucleotide sequence, provided that the  
fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
about 10 and about 100 nucleotides in length.
5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
25 about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and  
about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and  
30 about 40 bases in length.

9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.
10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
  - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

5 15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said  
10 polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;

b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;

c) a complementary nucleotide sequence comprising a sequence  
15 complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic  
20 sequence.

16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.

25 17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.

18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

30 19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS:

1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;  
and

b) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.

22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.

23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a nucleic acid from said subject;

b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;  
and

c) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.



24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

a) providing a first nucleic acid and a second nucleic acid;

b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and

d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.

25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.

27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.

28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.

29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group

consisting of polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising  
a) providing a protein sample from said subject;

b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and  
c) detecting said antibody-antigen complexes,  
whereby the presence of said complexes indicates the presence of said polypeptide.

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36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

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a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

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b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele, thereby treating said subject.

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37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

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38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 7867, or its complement; and

30

b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic

sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.

40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence,

thereby treating said subject.

41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867;

- b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867; and
- d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

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42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.

15 44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.